



Cura 468 SEQ list 0705
SEQUENCE LISTING



<110> Guo, Xiaojia
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<140> 09/981,151
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<213> Homo sapiens

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<223> Wherein n is an a or t or c or g.

<220>

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<222> (2383)

<223> Wherein n is an a or t or c or g.

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<222> (2983)

<223> wherein n is an a or t or c or g.

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 <223> wherein Xaa is any amino acid.

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 35 40 45
 Leu Ser Arg Gly Pro Arg Arg Leu Thr Ala Met Ser Pro Leu Phe Ser
 50 55 60
 Ala Gly Thr Cys Val Arg His Gly Thr Arg Ser Gly Ser Ala Trp Glu
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 Pro Glu Arg Pro Ala Ser Ser Ser Thr Arg Gly Ala Ala Gly Leu Asp
 85 90 95
 Gly Lys Gly Arg Asp Met Asp Glu Ala Gly Asn His Arg Ser Gln Gln
 100 105 110
 Thr Asn Thr Gly Thr Glu Asn Gln Thr Leu His Val Leu Thr Gln Tyr
 115 120 125
 Asp Leu Val Ser Ala Tyr Glu Val Asp His Arg Gly Asp Tyr Val Ser
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 His Glu Ile Met His His Gln Arg Arg Arg Arg Ala Val Ala Val Ser
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 Glu Val Glu Ser Leu His Leu Arg Leu Lys Gly Pro Arg His Asp Phe
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 His Met Asp Leu Arg Thr Ser Ser Ser Leu Val Ala Pro Gly Phe Ile
 180 185 190
 Val Gln Thr Leu Gly Lys Thr Gly Thr Lys Ser Val Gln Thr Leu Pro
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 Pro Glu Asp Phe Cys Phe Tyr Gln Gly Ser Leu Arg Ser His Arg Asn

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210

215

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Tyr Lys Trp Lys Pro Tyr Thr Gln Val Glu Xaa Asp Leu Cys Lys Leu
275 280 285
Tyr Cys Ile Ala Glu Gly Phe Asp Phe Phe Phe Ser Leu Ser Asn Lys
290 295 300
Val Lys Asp Gly Thr Pro Cys Ser Glu Asp Ser Arg Asn Val Cys Ile
305 310 315 320
Asp Gly Ile Cys Glu Leu Ser Val Val Ser Thr Ser Ala His Met Pro
325 330 335
Gln Pro Pro Lys Glu Asp Leu Phe Ile Leu Pro Asp Glu Tyr Lys Ser
340 345 350
Cys Leu Arg His Lys Arg Ser Leu Leu Arg Ser His Arg Asn Glu Glu
355 360 365
Leu Asn Val Glu Thr Leu Val Val Val Asp Lys Lys Met Met Gln Asn
370 375 380
His Gly His Glu Asn Ile Thr Thr Tyr Val Leu Thr Ile Leu Asn Met
385 390 395 400
Val Ser Ala Leu Phe Lys Asp Gly Thr Ile Gly Gly Asn Ile Asn Ile
405 410 415
Ala Ile Val Gly Leu Ile Leu Leu Glu Asp Glu Gln Pro Gly Leu Val
420 425 430
Ile Ser His His Ala Asp His Thr Leu Ser Ser Phe Cys Gln Trp Gln
435 440 445
Ser Gly Leu Met Gly Lys Asp Gly Thr Arg His Asp His Ala Ile Leu
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465 470 475 480
Leu Gly Phe Ala Pro Ile Ser Gly Met Cys Ser Lys Tyr Arg Ser Cys
485 490 495
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530 535 540
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555

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Val Lys Glu Tyr Lys Tyr Pro Glu Lys Leu Pro Gly Glu Leu Tyr Asp
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660 665 670
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675 680 685
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690 695 700
Glu Gly Ser Thr Arg Thr Leu Lys Leu Cys Asn Ser Gln Lys Cys Pro
705 710 715
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725 730 735
Arg Arg Phe Arg Gly Arg His Tyr Lys Trp Lys Pro Gln Asp Leu Cys
740 745 750
Lys Leu Tyr Cys Ile Ala Glu Gly Phe Asp Phe Phe Phe Ser Leu Ser
755 760 765
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770 775 780
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785 790 795
Asp Ala Val Glu Asp Val Cys Gly Val Cys Asn Gly Asn Asn Ser Ala
805 810 815
Cys Thr Ile His Arg Gly Leu Tyr Thr Lys His His His Thr Asn His
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Tyr His Met Val Thr Ile Pro Ser Gly Ala Arg Ser Ile Arg Ile Tyr
835 840 845
Glu Met Asn Val Ser Thr Ser Tyr Ile Ser Val Arg Asn Ala Leu Arg
850 855 860
Arg Tyr Tyr Leu Asn Gly His Trp Thr Val Asp Trp Pro Gly Arg Tyr
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Lys Phe Ser Gly Thr Thr Phe Asp Tyr Arg Arg Ser Tyr Asn Glu Pro

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885

890

895

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 Pro Arg Leu Gly Thr Glu Lys Gln Pro Pro Ala Gln Pro Ser Tyr Thr
 930 935 940
 Trp Ala Ile Val Arg Ser Glu Cys Ser Val Ser Cys Gly Gly Gly Arg
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 <213> Homo sapiens

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 <212> PRT
 <213> Homo sapiens

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Leu Ser Arg Gly Pro Arg Arg Leu Thr Ala Met Ser Pro Leu Phe Ser
  50          55          60
Ala Gly Thr Cys Val Arg His Gly Thr Arg Ser Gly Ser Ala Trp Glu
  65          70          75          80
Pro Glu Arg Pro Ala Ser Ser Ser Thr Arg Gly Ala Ala Gly Leu Asp
          85          90          95
Gly Lys Gly Arg Asp Met Asp Glu Ala Gly Asn His Arg Ser Gln Gln
          100          105          110
Thr Asn Thr Gly Thr Glu Asn Gln Thr Leu His Val Leu Thr Arg Glu
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Tyr Asp Leu Val Ser Ala Tyr Glu Val Asp His Arg Gly Asp Tyr Val
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Phe His Met Asp Leu Arg Thr Ser Ser Ser Leu Val Ala Pro Gly Phe
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Ile Val Gln Thr Leu Gly Lys Thr Gly Thr Lys Ser Val Gln Thr Leu
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Pro Pro Glu Asp Phe Cys Phe Tyr Gln Gly Ser Leu Arg Ser His Arg
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Glu Asp Val Cys Gly Val Cys Asn Gly Asn Asn Ser Ala Cys Thr Ile
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675 680 685
Gly Thr Thr Phe Asp Tyr Arg Arg Ser Tyr Asn Glu Pro Glu Asn Leu
690 695 700
Ile Ala Thr Gly Pro Thr Asn Glu Thr Leu Ile Val Glu Leu Leu Phe
705 710 715 720
Gln Gly Arg Asn Pro Gly Val Ala Trp Glu Tyr Ser Met Pro Arg Leu
725 730 735
Gly Thr Glu Lys Gln Pro Pro Ala Gln Pro Ser Tyr Thr Trp Ala Ile
740 745 750
Val Arg Ser Glu Cys Ser Val Ser Cys Gly Gly Gly Arg Cys Leu Pro
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Cura 468 SEQ list 0705

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 Ser Lys Arg Ile Ile Thr Asn Ala Met Leu Gly Glu Ser Ala Leu Ala
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Cura 468 SEQ list 0705
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Val Ile Ser His His Ala Asp His Thr Leu Ser Ser Phe Cys Gln Trp
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Cura 468 SEQ list 0705
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Cura 468 SEQ list 0705

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815

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Cura 468 SEQ list 0705

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Cura 468 SEQ list 0705

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Cura 468 SEQ list 0705

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Cura 468 SEQ list 0705

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<210> 10

<211> 1492

<212> PRT

<213> Homo sapiens

<400> 10

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Asp Val Lys Phe Thr Val Thr Leu Glu Thr Lys Asp Lys Thr Gln Lys
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Leu Leu Glu Tyr Ser Gly Leu Lys Lys Arg His Leu His Cys Ile Ser
  65             70             75             80
Phe Leu Val Pro Pro Pro Ala Gly Gly Thr Glu Glu Val Ala Thr Ile
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 115            120            125
Pro Leu Tyr Thr Pro Gly Gln Gln Val Tyr Phe Arg Ile Val Thr Met
 130            135            140
Asp Ser Asn Phe Val Pro Val Asn Asp Lys Tyr Ser Met Val Glu Leu
 145            150            155            160
Gln Asp Pro Asn Ser Asn Arg Ile Ala Gln Trp Leu Glu Val Val Pro
 165            170            175

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 Phe Ser Val Glu Glu Tyr Val Leu Ser Pro Phe Leu Leu Leu Ser
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 Tyr Gly Lys Pro Met Leu Gly Ala Val Gln Val Ser Val Cys Gln Lys
 260 265 270
 Ala Asn Thr Tyr Trp Tyr Arg Glu Val Glu Arg Glu Gln Leu Pro Asp
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 Glu Thr Ser Gly Trp Asn Gly Thr Asp Val Ser Leu Glu Gly Lys Phe
 420 425 430
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 450 455 460
 Phe Leu Gly Ile His Arg Leu Asn Gly Pro Leu Lys Cys Gly Gln Pro
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 Gln Glu Val Leu Val Asp Tyr Tyr Ile Asp Pro Ala Asp Ala Ser Pro
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 Asp Gln Glu Ile Ser Phe Ser Tyr Tyr Leu Ile Gly Lys Gly Ser Leu
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Cura 468 SEQ list 0705

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 Pro Ser Leu Val Ile Tyr Ala Ile Phe Pro Ser Gly Gly Val Val Ala
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 Asp Lys Ile Gln Phe Ser Val Glu Met Cys Phe Asp Asn Gln Gln Leu
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 Pro Gly Ala Glu Val Glu Leu Gln Leu Gln Ala Ala Pro Gly Ser Leu
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 Cys Ala Leu Arg Ala Val Asp Glu Ser Val Leu Leu Leu Arg Pro Asp
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 690 695 700
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 805 810 815
 Asn Tyr Leu Lys Asp Cys Ile Arg Val Gln Thr Asp Leu Ala Lys Ser
 820 825 830
 His Glu Tyr Gln Leu Glu Ser Trp Ala Asp Ser Gln Thr Ser Ser Cys
 835 840 845

Cura 468 SEQ list 0705

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 Lys Leu Gly His Ile Asn Phe Thr Ile Ser Thr Lys Ile Leu Asp Ser
 865 870 875 880
 Asn Glu Pro Cys Gly Gly Gln Lys Gly Phe Val Pro Gln Lys Gly Arg
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 Ser Asp Thr Leu Ile Lys Pro Val Leu Val Lys Pro Glu Gly Val Leu
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 945 950 955 960
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 1140 1145 1150
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 1155 1160 1165
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 1170 1175 1180

Cura 468 SEQ list 0705

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Lys Glu Ile Ala Lys Ala Thr Ser Ile Val Ala Trp Leu Ala Lys Gln
1220 1225 1230

His Asn Ala Tyr Gly Gly Phe Ser Ser Thr Gln Asp Thr Val Val Ala
1235 1240 1245

Leu Gln Ala Leu Ala Lys Tyr Ala Thr Thr Ala Tyr Met Pro Ser Glu
1250 1255 1260

Glu Ile Asn Leu Val Val Lys Ser Thr Glu Asn Phe Gln Arg Thr Phe
1265 1270 1275 1280

Asn Ile Gln Ser Val Asn Arg Leu Val Phe Gln Gln Asp Thr Leu Pro
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Asn Val Pro Gly Met Tyr Thr Leu Glu Ala Ser Gly Gln Gly Cys Val
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Tyr Val Gln Thr Val Leu Arg Tyr Asn Ile Leu Pro Pro Thr Asn Met
1315 1320 1325

Lys Thr Phe Ser Leu Ser Val Glu Ile Gly Lys Ala Arg Cys Glu Gln
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Pro Thr Ser Pro Arg Ser Leu Thr Leu Thr Ile His Thr Ser Tyr Val
1345 1350 1355 1360

Gly Ser Arg Ser Ser Ser Asn Met Ala Ile Val Glu Val Lys Met Leu
1365 1370 1375

Ser Gly Phe Ser Pro Met Glu Gly Thr Asn Gln Leu Leu Leu Gln Gln
1380 1385 1390

Pro Leu Val Lys Lys Val Glu Phe Gly Thr Asp Thr Leu Asn Ile Tyr
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1410 1415 1420

Gln Ser Val Leu Val Thr Asn Leu Lys Pro Ala Thr Ile Lys Val Tyr
1425 1430 1435 1440

Asp Tyr Tyr Leu Pro Gly Ser Phe Lys Leu Ser Gln Tyr Thr Ile Val
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Trp Ser Met Asn Asn Asp Ser Ile Val Asp Ser Val Ala Arg His Pro
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Cura 468 SEQ list 0705

<212> DNA

<213> Homo sapiens

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<210> 12

<211> 326

<212> PRT

<213> Homo sapiens

<400> 12

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 35          40          45
Leu Gly Cys Ser Val Glu Ile Arg Lys Leu Trp Ser His Ile Arg Arg
 50          55          60
Pro Trp Gly Ile Ala Val Gly Leu Leu Cys Gln Phe Gly Leu Met Pro
 65          70          75          80
Phe Thr Ala Tyr Leu Leu Ala Ile Ser Phe Ser Leu Lys Pro Val Gln
 85          90          95
Ala Ile Ala Val Leu Ile Met Gly Cys Cys Arg Gly Ala Pro Ser Leu
100          105          110
Thr Phe Ser Pro Ser Gly Leu Met Glu Ile Trp Ile Ser Gly Ala Leu
115          120          125
Gly Met Met Pro Leu Cys Ile Tyr Leu Tyr Thr Trp Ser Trp Ser Leu
130          135          140
Gln Gln Asn Leu Thr Ile Pro Tyr Gln Asn Ile Gly Leu Ser Leu Gly
145          150          155          160
Ile Thr Leu Val Cys Leu Thr Ile Pro Val Ala Phe Gly Val Tyr Val
165          170          175
Asn Tyr Arg Trp Pro Lys Gln Ser Lys Ile Ile Leu Lys Ala Val Val

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Cura 468 SEQ list 0705
185 190

180

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Phe Pro Leu Ile Gly His Val Thr Gly Phe Leu Leu Ala Leu Phe Thr
225 230 235 240
His Gln Ser Trp Gln Arg Thr Leu Pro Ile Phe Leu Gly Leu Ala Phe
245 250 255
Lys Thr Pro Cys Asp Thr Leu Leu Ala Met Thr Ser Cys Pro Glu Cys
260 265 270
Ser Arg Leu Ile Tyr Ala Phe Ile Pro Leu Leu Tyr Gly Leu Phe Gln
275 280 285
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Pro Lys Gln Pro Arg Ile
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<211> 850
<212> DNA
<213> Homo sapiens

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<212> PRT
<213> Homo sapiens

<400> 14
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Val Val Gly Lys Gly Thr His Cys Leu Ile Pro Trp Leu Gln Lys Ser
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Ile Ile Phe Asp Cys Arg Ser Gln Pro Arg Asn Val Pro Val Ile Thr
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Gly Ser Lys Asp Leu Gln Asn Val Asn Leu Thr Leu Arg Ile Ile Phe
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Arg Pro Val Ala Ser Gln Leu Pro His Ile Phe Thr Ser Ser Gly Glu
100 105 110
Asp His Asp Glu Arg Val Pro Pro Ser Ile Thr Asn Lys Ile Leu Lys
115 120 125
Ser Val Val Ala Arg Phe Glu Ala Gly Glu Leu Ile Thr Gln Arg Glu
130 135 140
Gln Ile Ser Arg Gln Val Ser Asp Asp Leu Thr Glu Pro Ala Ala Thr
145 150 155 160
Phe Gly Leu Ile Leu Asp Asp Val Ser Leu Thr Tyr Leu Thr Phe Gly
165 170 175
Lys Glu Phe Ile Glu Ala Val Glu Ala Lys Gln Ile Ala Gln Gln Glu
180 185 190
Ala Glu Arg Ala Arg Phe Val Val Glu Lys Ala Glu Gln Gln Lys Lys
195 200 205
Ala Ala Ile Ile Ser Ala Glu Gly Asp Ser Lys Val Ala Glu Leu Ile
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225 230 235 240
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<213> Homo sapiens

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<210> 16

<211> 666

<212> PRT

<213> Homo sapiens

<400> 16

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Pro Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Val Leu Arg Gly Thr
      20              25              30

Glu Leu Gln His Leu Leu His Ala Val Val Pro Gly Pro Trp Gln Glu
 35              40              45

Asp Val Ala Asp Ala Glu Glu Cys Ala Gly Arg Cys Gly Pro Leu Met
 50              55              60

Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln Leu
 65              70              75              80

Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg Arg Ser Gly
      85              90              95

Arg Cys Asp Leu Phe Gln Lys Lys Asp Tyr Val Arg Thr Cys Ile Met
 100              105              110

Asn Asn Gly Val Gly Tyr Arg Gly Thr Met Ala Thr Thr Val Gly Gly
 115              120              125

Leu Pro Cys Gln Ala Trp Ser His Lys Phe Pro Asn Asp His Lys Tyr
 130              135              140

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Thr Pro Thr Leu Arg Asn Gly Leu Glu Glu Asn Phe Cys Arg Asn Pro
 145 150 155 160
 Asp Gly Asp Pro Gly Gly Pro Trp Cys Tyr Thr Thr Asp Pro Ala Val
 165 170 175
 Arg Phe Gln Ser Cys Gly Ile Lys Ser Cys Arg Glu Ala Ala Cys Val
 180 185 190
 Trp Cys Asn Gly Glu Glu Tyr Arg Gly Ala Val Asp Arg Thr Glu Ser
 195 200 205
 Gly Arg Glu Cys Gln Arg Trp Asp Leu Gln His Pro His Gln His Pro
 210 215 220
 Phe Glu Pro Gly Lys Phe Leu Asp Gln Gly Leu Asp Asp Asn Tyr Cys
 225 230 235 240
 Arg Asn Pro Asp Gly Ser Glu Arg Pro Trp Cys Tyr Thr Thr Asp Pro
 245 250 255
 Gln Ile Glu Arg Glu Phe Cys Asp Leu Pro Arg Cys Gly Ser Glu Ala
 260 265 270
 Gln Pro Arg Gln Glu Ala Thr Thr Val Ser Cys Phe Arg Gly Lys Gly
 275 280 285
 Glu Gly Tyr Arg Gly Thr Ala Asn Thr Thr Thr Ala Gly Val Pro Cys
 290 295 300
 Gln Arg Trp Asp Ala Gln Ile Pro His Gln His Arg Phe Thr Pro Glu
 305 310 315 320
 Lys Tyr Ala Cys Lys Asp Leu Arg Glu Asn Phe Cys Arg Asn Pro Asp
 325 330 335
 Gly Ser Glu Ala Pro Trp Cys Phe Thr Leu Arg Pro Gly Met Arg Ala
 340 345 350
 Ala Phe Cys Tyr Gln Ile Arg Arg Cys Thr Asp Asp Val Arg Pro Gln
 355 360 365
 Thr Ala Thr Thr Ala Gln Gly Ser Ser Thr Ala Ala Arg Ser Ala Arg
 370 375 380
 Pro Ala Arg Val Ser Ser Ala Ser Ala Gly Pro Leu Arg Arg Arg Thr
 385 390 395 400
 Ser Arg Ser Ser Arg Leu Pro Pro Asn Arg Met His Asn Trp Arg Arg
 405 410 415
 Thr Ser Ala Gly Thr Gln Met Gly Ile Ala Met Gly Pro Gly Ala Thr
 420 425 430
 Arg Trp Thr Gln Gly Pro His Ser Thr Thr Val Pro Cys Asp Ala Ala
 435 440 445
 Leu Met Thr Ser Arg His Gln Ser Trp Thr Pro Gln Thr Arg Cys Ser
 450 455 460
 Leu Arg Ser Val Ala Arg Gly Trp Ile Gly Trp Ile Ser Gly Val Pro
 465 470 475 480

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Ser Cys Ala Trp Leu Gly Ala Ile Arg Ala Thr His Pro Gly Gln Ser
485 490 495

Ala Cys Gly Ile Gly Met Leu Pro Leu Thr Gly Tyr Glu Val Trp Leu
500 505 510

Gly Thr Leu Phe Gln Asn Pro Gln His Gly Glu Pro Ser Leu Gln Arg
515 520 525

Val Pro Val Ala Lys Met Val Cys Gly Pro Ser Gly Ser Gln Leu Val
530 535 540

Leu Leu Lys Leu Glu Arg Ser Val Thr Leu Asn Gln Arg Val Ala Leu
545 550 555 560

Ile Cys Leu Pro Pro Glu Trp Tyr Val Val Pro Pro Gly Thr Lys Cys
565 570 575

Glu Ile Ala Gly Trp Gly Glu Thr Lys Gly Thr Gly Asn Asp Thr Val
580 585 590

Leu Asn Val Ala Leu Leu Asn Val Ile Ser Asn Gln Glu Cys Asn Ile
595 600 605

Lys His Arg Gly Arg Gly Asp Tyr Gly Gly Pro Leu Ala Cys Phe Thr
610 615 620

His Asn Cys Trp Val Leu Glu Gly Ile Ile Ile Pro Asn Arg Val Cys
625 630 635 640

Ala Arg Ser Cys Trp Pro Ala Val Phe Thr Arg Val Ser Val Phe Val
645 650 655

Asp Trp Ile His Lys Val Met Arg Leu Gly
660 665

<210> 17
<211> 634
<212> DNA
<213> Homo sapiens

<400> 17
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gccacagtgc agcagctggg aggaagatgg cgcctggtgg acagcaaagc ctttgatgaa 120
tacatgaagg agggaggagt gggaaactgct ttgcgaaaaa tggacgcaat ggccaagcca 180
gattgtatca tcaacttgta tggcaaaaac ctcaccataa aaaccgagag cactttgaaa 240
acacagtttt cttgtaccct gggagagaag tttgaagaaa ccacagctga tggcagaaaa 300
actcagactg tgtgcagctt tgcagatggt gcattgggtc agcatcagga gtgggatggg 360
aaggaaaaca caataacaag aaaactgaaa gatgggaaat tagtgggtgta ctgtgtcatg 420
aacaatgtcg cctgtactcg gatctatgaa aaagtagaat aaaaattcca tcatcacttt 480
ggacaggagt taactaatag aatgatcaag ctcagttcaa tgagcaaadc tccatagtgt 540
tttttttcat tactgtgttc aattatcttt atcacaaacg tttcacatgc agctattttca 600
aagtgtcttg gattaattag gatcatccct ttgg 634

<210> 18
<211> 134
<212> PRT
<213> Homo sapiens

<400> 18
Met Ala Thr Val Gln Gln Leu Gly Gly Arg Trp Arg Leu Val Asp Ser

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 Lys Arg Phe Asp Glu Tyr Met Lys Glu Gly Gly Val Gly Thr Ala Leu
 20 25 30
 Arg Lys Met Asp Ala Met Ala Lys Pro Asp Cys Ile Ile Thr Cys Asp
 35 40 45
 Gly Lys Asn Leu Thr Ile Lys Thr Glu Ser Thr Leu Lys Thr Gln Phe
 50 55 60
 Ser Cys Thr Leu Gly Glu Lys Phe Glu Glu Thr Thr Ala Asp Gly Arg
 65 70 75 80
 Lys Thr Gln Thr Val Cys Ser Phe Ala Asp Gly Ala Leu Val Gln His
 85 90 95
 Gln Glu Trp Asp Gly Lys Glu Asn Thr Ile Thr Arg Lys Leu Lys Asp
 100 105 110
 Gly Lys Leu Val Val Tyr Cys Val Met Asn Asn Val Ala Cys Thr Arg
 115 120 125
 Ile Tyr Glu Lys Val Glu
 130

<210> 19
 <211> 822
 <212> DNA
 <213> Homo sapiens

<400> 19
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 ggaggagggtg tgggacgatg agcagaagga ctttgtctgc aacaccaagc agcccggctg 180
 ccccaacgtc tgctatgacg agttcttccc cgtgtccac gtgcgcctct gggccctaca 240
 gctcatcctg gtcacgtgcc cctcactgct cgtgggtcatg cacgtggcct accgcgagga 300
 acgcgagcgc aagcaccacc tgaaacacgg gcccaatgcc ccgtccctgt acgacaacct 360
 gagcaagaag cggggcggac tgtgggtggac gtacttgctg agcctcatct tcaaggccgc 420
 cgtggatgct ggcttcctct atatcttcca ccgcctctac aaggattatg acatgccccg 480
 cgtgggtggc tgctccgtgg agccttgccc ccacactgtg gactgttaca tctcccggcc 540
 cacggagaag aaggtcttca cctacttcat ggtgaccaca gctgccatct gcacccctgt 600
 caacctcagt gaagtcttct acctgggtgg caagagggtg atggagatct tcggccccag 660
 gcaccggcgt cctcgggtgcc gggaatgcct acccgatacg tgcccaccat atgtcctctc 720
 ccaggagggt caccctgagg atgggaactc tgtcctaata aaggctgggt cggccccagt 780
 ggatgcaggt gggatatccat aacctgcgag atcagcagat aa 822

<210> 20
 <211> 266
 <212> PRT
 <213> Homo sapiens

<400> 20
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 1 5 10 15
 Ser Thr Val Leu Ser Arg Ile Trp Leu Ser Val Val Phe Ile Phe Arg
 20 25 30
 Val Leu Val Tyr Val Val Ala Ala Glu Glu Val Trp Asp Asp Glu Gln
 35 40 45

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Lys Asp Phe Val Cys Asn Thr Lys Gln Pro Gly Cys Pro Asn Val Cys
50 55 60
Tyr Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln
65 70 75 80
Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala
85 90 95
Tyr Arg Glu Glu Arg Glu Arg Lys His His Leu Lys His Gly Pro Asn
100 105 110
Ala Pro Ser Leu Tyr Asp Asn Leu Ser Lys Lys Arg Gly Gly Leu Trp
115 120 125
Trp Thr Tyr Leu Leu Ser Leu Ile Phe Lys Ala Ala Val Asp Ala Gly
130 135 140
Phe Leu Tyr Ile Phe His Arg Leu Tyr Lys Asp Tyr Asp Met Pro Arg
145 150 155 160
Val Val Ala Cys Ser Val Glu Pro Cys Pro His Thr Val Asp Cys Tyr
165 170 175
Ile Ser Arg Pro Thr Glu Lys Lys Val Phe Thr Tyr Phe Met Val Thr
180 185 190
Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Ser Glu Val Phe Tyr Leu
195 200 205
Val Gly Lys Arg Cys Met Glu Ile Phe Gly Pro Arg His Arg Arg Pro
210 215 220
Arg Cys Arg Glu Cys Leu Pro Asp Thr Cys Pro Pro Tyr Val Leu Ser
225 230 235 240
Gln Gly Gly His Pro Glu Asp Gly Asn Ser Val Leu Met Lys Ala Gly
245 250 255
Ser Ala Pro Val Asp Ala Gly Gly Tyr Pro
260 265

<210> 21
<211> 546
<212> DNA
<213> Homo sapiens

<400> 21
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tgtgaactaa atccacagcc acataataat caaaacagaa aagcaaaaga aagccacttc 180
aggaaatacc acggctcacac ctccagttggc ttcatgctac agattataga aaatatgttg 240
ctgcccgggc caccaatctg ttgggttcaca ttactacgtg agcaatgtaa gtgtttgcaa 300
gaagccatcc actatctaaa tatcagatat agatgctcca aagcagctac gtcagtgatg 360
agaacagaga aaatacgtag caacatttca ttaagttgaa ttctaatact taaaaggctc 420
cttttagtac tgacattctg gattttaaaa gttatgttga ccgcatgttc tactcaciaa 480
gtgggagttg aacaatgaga acacacggac acgggggaagg gaacatcaca caccagggcc 540
gtcag 546

<210> 22

Cura 468 SEQ list 0705

<211> 61
 <212> PRT
 <213> Homo sapiens

<400> 22
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 1 5 10 15
 Trp Phe Thr Leu Leu Arg Glu Gln Cys Lys Cys Leu Gln Glu Ala Ile
 20 25 30
 His Tyr Leu Asn Ile Arg Tyr Arg Cys Ser Lys Ala Ala Thr Ser Val
 35 40 45
 Met Arg Thr Glu Lys Ile Arg Ser Asn Ile Ser Leu Ser
 50 55 60

<210> 23
 <211> 2309
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (2196)
 <223> wherein n is an a o t or c or g.

<400> 23
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 acaagcatac acaatgggga attgacttct tggaagata tgccaaattt gttaaagaga 180
 ggatagaaat tgaacagaac tatgcgaaac aattgagaaa tctggttaag aagtactgcc 240
 ccaaacgttc atccaaagat gaagagccac ggtttacctc gtgtgtagcc tttttaata 300
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 atctgcaaga aggacgaaaa gctcaacaat atcttgacat gtgctggaag cagatgggta 480
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 ttttatttta ttgctgtcta atcaataaag aatgcagagc tgtcaaaaaa tgtgtcttac 2040

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atttagctgt cccaacagga ttgtcttccc tcccagctct gggttttaatt ggcttttaga 2100
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cctaacatcc tgttgcatgt ctagcgtgat tgagcnagat tttcaggcat gtccttagaa 2220
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<210> 24
 <211> 547
 <212> PRT
 <213> Homo sapiens

<400> 24
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 20 25 30
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 35 40 45
 Leu Val Lys Lys Tyr Cys Pro Lys Arg Ser Ser Lys Asp Glu Glu Pro
 50 55 60
 Arg Phe Thr Ser Cys Val Ala Phe Phe Asn Ile Leu Asn Glu Leu Asn
 65 70 75 80
 Asp Tyr Ala Gly Gln Arg Glu Val Val Ala Glu Glu Met Ala His Arg
 85 90 95
 Val Tyr Gly Glu Leu Met Arg Tyr Ala His Asp Leu Lys Thr Glu Arg
 100 105 110
 Lys Met His Leu Gln Glu Gly Arg Lys Ala Gln Gln Tyr Leu Asp Met
 115 120 125
 Cys Trp Lys Gln Met Gly Asn Ser Lys Lys Lys Phe Glu Arg Glu Cys
 130 135 140
 Arg Glu Ala Glu Lys Ala Gln Gln Ser Tyr Glu Arg Leu Asp Asn Asp
 145 150 155 160
 Thr Asn Ala Thr Lys Ala Asp Val Glu Asn Ala Lys Gln Gln Leu Asn
 165 170 175
 Leu Arg Thr His Met Ala Asp Glu Asn Lys Asn Ala Tyr Ala Ala Gln
 180 185 190
 Leu Gln Asn Phe Asn Gly Glu Gln His Lys His Phe Tyr Val Val Ile
 195 200 205
 Pro Gln Ile Tyr Lys Gln Leu Gln Glu Met Asp Glu Arg Arg Thr Ile
 210 215 220
 Lys Leu Ser Glu Cys Tyr Arg Gly Phe Ala Asp Ser Glu Arg Lys Val
 225 230 235 240
 Ile Pro Ile Ile Ser Lys Cys Leu Glu Gly Met Ile Leu Ala Ala Lys
 245 250 255
 Ser Val Asp Glu Arg Arg Asp Ser Gln Met Val Val Asp Ser Phe Lys
 260 265 270

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Ser Gly Phe Glu Pro Pro Gly Asp Phe Pro Phe Glu Asp Tyr Ser Gln
275 280 285
His Ile Tyr Arg Thr Ile Ser Asp Gly Thr Ile Ser Ala Ser Lys Gln
290 295 300
Glu Ser Gly Lys Met Asp Ala Lys Thr Pro Val Gly Lys Ala Lys Gly
305 310 315 320
Lys Leu Trp Leu Phe Gly Lys Lys Pro Lys Gly Pro Ala Leu Glu Asp
325 330 335
Phe Ser His Leu Pro Pro Glu Gln Arg Arg Lys Lys Leu Gln Gln Arg
340 345 350
Ile Asp Glu Leu Asn Arg Glu Leu Gln Lys Glu Ser Asp Gln Lys Asp
355 360 365
Ala Leu Asn Lys Met Lys Asp Val Tyr Glu Lys Asp Pro Gln Met Gly
370 375 380
Asp Pro Gly Ser Leu Gln Pro Lys Leu Ala Glu Thr Met Asn Asn Ile
385 390 395 400
Asp Arg Leu Arg Met Glu Ile His Lys Asn Glu Ala Trp Leu Ser Glu
405 410 415
Val Glu Gly Lys Thr Gly Gly Arg Gly Asp Arg Arg His Ser Ser Asp
420 425 430
Ile Asn His Leu Val Thr Gln Gly Arg Glu Ser Pro Glu Gly Ser Tyr
435 440 445
Thr Asp Asp Ala Asn Gln Glu Val Arg Gly Pro Pro Gln Gln His Gly
450 455 460
His His Asn Glu Phe Asp Asp Glu Phe Glu Asp Asp Asp Pro Leu Pro
465 470 475 480
Ala Ile Gly His Cys Lys Ala Ile Tyr Pro Phe Asp Gly His Asn Glu
485 490 495
Gly Thr Leu Ala Met Lys Glu Gly Glu Val Leu Tyr Ile Ile Glu Glu
500 505 510
Asp Lys Gly Asp Gly Trp Thr Arg Ala Arg Arg Gln Asn Gly Glu Glu
515 520 525
Gly Tyr Val Pro Thr Ser Tyr Ile Asp Val Thr Leu Glu Lys Asn Ser
530 535 540
Lys Gly Ser
545

<210> 25
<211> 1787
<212> DNA
<213> Homo sapiens

<400> 25
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<210> 26

<211> 1787

<212> DNA

<213> Homo sapiens

<400> 26

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gcacactagg	gggccccgc	tatctccctg	gcatgcatca	gccccctcgt	ccaggtagcc	540
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gagctgagca	aactcctggg	aactgttgag	tttgatgtca	gtgaggttta	ctcccttggtg	1260
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<210> 27
 <211> 472
 <212> PRT
 <213> Homo sapiens

<400> 27
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 Glu Glu Gly Pro Gly Pro Gly Ile Phe Arg Ala Glu Pro Gly Asp Gln
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 Gln His Pro Ile Ser Gln Ala Val Cys Trp Arg Ser Met Arg Arg Gly
 35 40 45
 Cys Ala Val Leu Gly Ala Leu Gly Leu Leu Ala Gly Ala Gly Val Gly
 50 55 60
 Ser Trp Leu Leu Val Leu Tyr Leu Cys Pro Ala Ala Ser Gln Pro Ile
 65 70 75 80
 Ser Gly Thr Leu Gln Asp Glu Glu Ile Thr Leu Ser Cys Ser Glu Ala
 85 90 95
 Ser Ala Glu Glu Ala Leu Leu Pro Ala Leu Pro Lys Thr Val Ser Phe
 100 105 110
 Arg Ile Asn Ser Glu Asp Phe Leu Leu Glu Ala Gln Val Arg Asp Gln
 115 120 125
 Pro Arg Trp Leu Leu Val Cys His Glu Gly Trp Ser Pro Ala Leu Gly
 130 135 140
 Leu Gln Ile Cys Trp Ser Leu Gly His Leu Arg Leu Thr His His Lys
 145 150 155 160
 Gly Val Asn Leu Thr Asp Ile Lys Leu Asn Ser Ser Gln Glu Phe Ala
 165 170 175
 Gln Leu Ser Pro Arg Leu Gly Gly Phe Leu Glu Glu Ala Trp Gln Pro
 180 185 190
 Ser Arg Thr Thr Glu Ala Val Arg Asn Asn Cys Thr Ser Gly Gln Val
 195 200 205
 Val Ser Leu Arg Cys Ser Glu Cys Gly Ala Arg Pro Leu Ala Ser Arg
 210 215 220
 Ile Val Gly Gly Gln Ser Val Ala Pro Gly Arg Trp Pro Trp Gln Ala
 225 230 235 240
 Ser Val Ala Leu Gly Phe Arg His Thr Cys Gly Gly Ser Val Leu Ala
 245 250 255
 Pro Arg Trp Val Val Thr Ala Ala His Cys Met His Ser Phe Arg Leu
 260 265 270

Cura 468 SEQ list 0705

Ala Arg Leu Ser Ser Trp Arg Val His Ala Gly Leu Val Ser His Ser
 275 280 285

Ala Val Arg Pro His Gln Gly Ala Leu Val Glu Arg Ile Ile Pro His
 290 295 300

Pro Leu Tyr Ser Ala Gln Asn His Asp Tyr Asp Val Ala Leu Leu Arg
 305 310 315 320

Leu Gln Thr Ala Leu Asn Phe Ser Asp Thr Val Gly Ala Val Cys Leu
 325 330 335

Pro Ala Lys Glu Gln His Phe Pro Lys Gly Ser Arg Cys Trp Val Ser
 340 345 350

Gly Trp Gly His Thr His Pro Ser His Thr Tyr Ser Ser Asp Met Leu
 355 360 365

Gln Asp Thr Val Val Pro Leu Leu Ser Thr Gln Leu Cys Asn Ser Ser
 370 375 380

Cys Val Tyr Ser Gly Ala Leu Thr Pro Arg Met Leu Cys Ala Gly Tyr
 385 390 395 400

Leu Asp Gly Arg Ala Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu
 405 410 415

Val Cys Pro Asp Gly Asp Thr Trp Arg Leu Val Gly Val Val Ser Trp
 420 425 430

Gly Arg Gly Cys Ala Glu Pro Asn His Pro Gly Val Tyr Ala Lys Val
 435 440 445

Ala Glu Phe Leu Asp Trp Ile His Asp Thr Ala Gln Val Ser Val Gly
 450 455 460

Ala Gly Val Gly Gln Gly Asp Phe
 465 470

<210> 28

<211> 2148

<212> DNA

<213> Homo sapiens

<400> 28

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cccctatgga	ggcccagtat	gcagaggagg	gcccaggacc	tgggatcttc	agagcagagc	240
ctggagacca	gcagcatccc	atttctcagg	cggtgtgctg	gcgttccatg	cgacgtggct	300
gtgcagtgct	gggagccctg	gggctgctgg	ccggtgcagg	tggtggctca	tggtccttag	360
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taactttgag	ctgtctcagag	gccagcgctg	aggaagctct	gctccctgca	ctccccaaaa	480
cagtatcttt	cagaataaac	agcgaagact	tcttgctgga	agcgcaagtg	agggatcagc	540
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ggagccttgg	gcatctcaga	ctcactcacc	acaagggagt	aaacctcact	gacatcaaac	660
tcaacagttc	ccaggagttt	gctcagctct	ctcctagact	gggaggcttc	ctggaggagg	720
cgtggcagcc	caggaacaac	tgcacttctg	gtcaagttgt	ttccctcaga	tgctctgagt	780
gtggagcgag	gcccctggct	tcccggatag	ttgggtgggc	gtctgtggct	cctgggcgct	840
ggccgtggca	ggccagcgtg	gccctgggct	tccggcacac	gtgtgggggc	tctgtgctag	900
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acgtcgccct	cctgaggctc	cagaccgctc	tcaacttctc	agacactgtg	ggcgctgtgt	1020

Cura 468 SEQ list 0705

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gcctgccggc caaggaacag cattttccga agggctcgcg gtgctgggtg tccggctggt 1080
gccacaccca ccctagccat acttacagct cggatatgct ccaggacacg gtggtgcccc 1140
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gctgcgcaga gccaatcac ccaggtgtct acgccaagggt agctgagttt ctggactgga 1380
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acaccactgc ctcatgcttc ctggggcctc cagcagctcc actaatggag gagaggcagt 1500
agcctccgac acagaacgca tggacctcct actactgtgt gtgaggaaca gtcactacc 1560
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<210> 29

<211> 418

<212> PRT

<213> Homo sapiens

<400> 29

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Glu Glu Gly Pro Gly Pro Gly Ile Phe Arg Ala Glu Pro Gly Asp Gln
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Gln His Pro Ile Ser Gln Ala Val Cys Trp Arg Ser Met Arg Arg Gly
      35           40           45
Cys Ala Val Leu Gly Ala Leu Gly Leu Leu Ala Gly Ala Gly Val Gly
      50           55           60
Ser Trp Leu Leu Val Leu Tyr Leu Cys Pro Ala Ala Ser Gln Pro Ile
      65           70           75           80
Ser Gly Thr Leu Gln Asp Glu Glu Ile Thr Leu Ser Cys Ser Glu Ala
          85           90           95
Ser Ala Glu Glu Ala Leu Leu Pro Ala Leu Pro Lys Thr Val Ser Phe
      100           105           110
Arg Ile Asn Ser Glu Asp Phe Leu Leu Glu Ala Gln Val Arg Asp Gln
      115           120           125
Pro Arg Trp Leu Leu Val Cys His Glu Gly Trp Ser Pro Ala Leu Gly
      130           135           140
Leu Gln Ile Cys Trp Ser Leu Gly His Leu Arg Leu Thr His His Lys
      145           150           155           160
Gly Val Asn Leu Thr Asp Ile Lys Leu Asn Ser Ser Gln Glu Phe Ala
          165           170           175
Gln Leu Ser Pro Arg Leu Gly Gly Phe Leu Glu Glu Ala Trp Gln Pro
      180           185           190

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Cura 468 SEQ list 0705

Arg Asn Asn Cys Thr Ser Gly Gln Val Val Ser Leu Arg Cys Ser Glu
195 200 205
Cys Gly Ala Arg Pro Leu Ala Ser Arg Ile Val Gly Gly Gln Ser Val
210 215 220
Ala Pro Gly Arg Trp Pro Trp Gln Ala Ser Val Ala Leu Gly Phe Arg
225 230 235 240
His Thr Cys Gly Gly Ser Val Leu Ala Pro Arg Trp Val Val Thr Ala
245 250 255
Ala His Cys Met His Ser Ala Gln Asn His Asp Tyr Asp Val Ala Leu
260 265 270
Leu Arg Leu Gln Thr Ala Leu Asn Phe Ser Asp Thr Val Gly Ala Val
275 280 285
Cys Leu Pro Ala Lys Glu Gln His Phe Pro Lys Gly Ser Arg Cys Trp
290 295 300
Val Ser Gly Trp Cys His Thr His Pro Ser His Thr Tyr Ser Ser Asp
305 310 315 320
Met Leu Gln Asp Thr Val Val Pro Leu Leu Ser Thr Gln Leu Cys Asn
325 330 335
Ser Ser Cys Val Tyr Ser Gly Ala Leu Thr Pro Arg Met Leu Cys Ala
340 345 350
Gly Tyr Leu Asp Gly Arg Ala Asp Ala Cys Gln Gly Asp Ser Gly Gly
355 360 365
Pro Leu Val Cys Pro Asp Gly Asp Thr Trp Arg Leu Val Gly Val Val
370 375 380
Ser Trp Gly Arg Gly Cys Ala Glu Pro Asn His Pro Gly Val Tyr Ala
385 390 395 400
Lys Val Ala Glu Phe Leu Asp Trp Ile His Asp Thr Ala Gln Asp Ser
405 410 415
Leu Leu

<210> 30
<211> 1593
<212> PRT
<213> Homo sapiens

<400> 30
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Gln Leu Leu Asn Phe Gly Ala Leu Cys Tyr Gly Arg Gln Pro Gln Pro
20 25 30
Gly Pro Val Arg Phe Pro Asp Arg Arg Gln Glu His Phe Ile Lys Gly
35 40 45
Leu Pro Glu Tyr His Val Val Gly Pro Val Arg Val Asp Ala Ser Gly
50 55 60

Cura 468 SEQ list 0705

His Phe Leu Ser Tyr Gly Leu His Tyr Pro Ile Thr Ser Ser Arg Arg
 65 70 75 80
 Lys Arg Asp Leu Asp Gly Ser Glu Asp Trp Val Tyr Tyr Arg Ile Ser
 85 90 95
 His Glu Glu Lys Asp Leu Phe Phe Asn Leu Thr Val Asn Gln Gly Phe
 100 105 110
 Leu Ser Asn Ser Tyr Ile Met Glu Lys Arg Tyr Gly Asn Leu Ser His
 115 120 125
 Val Lys Met Met Ala Ser Ser Ala Pro Leu Cys His Leu Ser Gly Thr
 130 135 140
 Val Leu Gln Gln Gly Thr Arg Val Gly Thr Ala Ala Leu Ser Ala Cys
 145 150 155 160
 His Gly Leu Thr Gly Phe Phe Gln Leu Pro His Gly Asp Phe Phe Ile
 165 170 175
 Glu Pro Val Lys Lys His Pro Leu Val Glu Gly Gly Tyr His Pro His
 180 185 190
 Ile Val Tyr Arg Arg Gln Lys Val Pro Glu Thr Lys Glu Pro Thr Cys
 195 200 205
 Gly Leu Lys Asp Ser Val Asn Ile Ser Gln Lys Gln Glu Leu Trp Arg
 210 215 220
 Glu Lys Trp Glu Arg His Asn Leu Pro Ser Arg Ser Leu Ser Arg Arg
 225 230 235 240
 Ser Ile Ser Lys Glu Arg Trp Val Glu Thr Leu Val Val Ala Asp Thr
 245 250 255
 Lys Met Ile Glu Tyr His Gly Ser Glu Asn Val Glu Ser Tyr Ile Leu
 260 265 270
 Thr Ile Met Asn Met Val Thr Gly Leu Phe His Asn Pro Ser Ile Gly
 275 280 285
 Asn Ala Ile His Ile Val Val Val Arg Leu Ile Leu Leu Glu Glu Glu
 290 295 300
 Glu Gln Gly Leu Lys Ile Val His His Ala Glu Lys Thr Leu Ser Ser
 305 310 315 320
 Phe Cys Lys Trp Gln Lys Ser Ile Asn Pro Lys Ser Asp Leu Asn Pro
 325 330 335
 Val His His Asp Val Ala Val Leu Leu Thr Arg Lys Asp Ile Cys Ala
 340 345 350
 Gly Phe Asn Arg Pro Cys Glu Thr Leu Gly Leu Ser His Leu Ser Gly
 355 360 365
 Met Cys Gln Pro His Arg Ser Cys Asn Ile Asn Glu Asp Ser Gly Leu
 370 375 380
 Pro Leu Ala Phe Thr Ile Ala His Glu Leu Gly His Ser Phe Gly Ile
 385 390 395 400

Cura 468 SEQ list 0705

Gln His Asp Gly Lys Glu Asn Asp Cys Glu Pro Val Gly Arg His Pro
405 410 415

Tyr Ile Met Ser Arg Gln Leu Gln Tyr Asp Pro Thr Pro Leu Thr Trp
420 425 430

Ser Lys Cys Ser Glu Glu Tyr Ile Thr Arg Phe Leu Asp Arg Gly Trp
435 440 445

Gly Phe Cys Leu Asp Asp Ile Pro Lys Lys Lys Gly Leu Lys Ser Lys
450 455 460

Val Ile Ala Pro Gly Val Ile Tyr Asp Val His His Gln Cys Gln Leu
465 470 475 480

Gln Tyr Gly Pro Asn Ala Thr Phe Cys Gln Glu Val Glu Asn Val Cys
485 490 495

Gln Thr Leu Trp Cys Ser Val Lys Gly Phe Cys Arg Ser Lys Leu Asp
500 505 510

Ala Ala Ala Asp Gly Thr Gln Cys Gly Glu Lys Lys Trp Cys Met Ala
515 520 525

Gly Lys Cys Ile Thr Val Gly Lys Lys Pro Glu Ser Ile Pro Gly Gly
530 535 540

Trp Gly Arg Trp Ser Pro Trp Ser His Cys Ser Arg Thr Cys Gly Ala
545 550 555 560

Gly Val Gln Ser Ala Glu Arg Leu Cys Asn Asn Pro Glu Pro Lys Phe
565 570 575

Gly Gly Lys Tyr Cys Thr Gly Glu Arg Lys Arg Tyr Arg Leu Cys Asn
580 585 590

Val His Pro Cys Arg Ser Glu Ala Pro Thr Phe Arg Gln Met Gln Cys
595 600 605

Ser Glu Phe Asp Thr Val Pro Tyr Lys Asn Glu Leu Tyr His Trp Phe
610 615 620

Pro Ile Phe Asn Pro Ala His Pro Cys Glu Leu Tyr Cys Arg Pro Ile
625 630 635 640

Asp Gly Gln Phe Ser Glu Lys Met Leu Asp Ala Val Ile Asp Gly Thr
645 650 655

Pro Cys Phe Glu Gly Gly Asn Ser Arg Asn Val Cys Ile Asn Gly Ile
660 665 670

Cys Lys Met Val Gly Cys Asp Tyr Glu Ile Asp Ser Asn Ala Thr Glu
675 680 685

Asp Arg Cys Gly Val Cys Leu Gly Asp Gly Ser Ser Cys Gln Thr Val
690 695 700

Arg Lys Met Phe Lys Gln Lys Glu Gly Ser Gly Tyr Val Asp Ile Gly
705 710 715 720

Leu Ile Pro Lys Gly Ala Arg Asp Ile Arg Val Met Glu Ile Glu Gly
725 730 735

Cura 468 SEQ list 0705

Ala Gly Asn Phe Leu Ala Ile Arg Ser Glu Asp Pro Glu Lys Tyr Tyr
740 745 750

Leu Asn Gly Gly Phe Ile Ile Gln Trp Asn Gly Asn Tyr Lys Leu Ala
755 760 765

Gly Thr Val Phe Gln Tyr Asp Arg Lys Gly Asp Leu Glu Lys Leu Met
770 775 780

Ala Thr Gly Pro Thr Asn Glu Ser Val Trp Ile Gln Leu Leu Phe Gln
785 790 795 800

Val Thr Asn Pro Gly Ile Lys Tyr Glu Tyr Thr Ile Gln Lys Asp Gly
805 810 815

Leu Asp Asn Asp Val Glu Gln Met Tyr Phe Trp Gln Tyr Gly His Trp
820 825 830

Thr Glu Cys Ser Val Thr Cys Gly Thr Gly Ile Arg Arg Gln Thr Ala
835 840 845

His Cys Ile Lys Lys Gly Arg Gly Met Val Lys Ala Thr Phe Cys Asp
850 855 860

Pro Glu Thr Gln Pro Asn Gly Arg Gln Lys Lys Cys His Glu Lys Ala
865 870 875 880

Cys Pro Pro Arg Trp Trp Ala Gly Glu Trp Glu Ala Cys Ser Ala Thr
885 890 895

Cys Gly Pro His Gly Glu Lys Lys Arg Thr Val Leu Cys Ile Gln Thr
900 905 910

Met Val Ser Asp Glu Gln Ala Leu Pro Pro Thr Asp Cys Gln His Leu
915 920 925

Leu Lys Pro Lys Thr Leu Leu Ser Cys Asn Arg Asp Ile Leu Cys Pro
930 935 940

Ser Asp Trp Thr Val Gly Asn Trp Ser Glu Cys Ser Val Ser Cys Gly
945 950 955 960

Gly Gly Val Arg Ile Arg Ser Val Thr Cys Ala Lys Asn His Asp Glu
965 970 975

Pro Cys Asp Val Thr Arg Lys Pro Asn Ser Arg Ala Leu Cys Gly Leu
980 985 990

Gln Gln Cys Pro Ser Ser Arg Arg Val Leu Lys Pro Asn Lys Gly Thr
995 1000 1005

Ile Ser Asn Gly Lys Asn Pro Pro Thr Leu Lys Pro Val Pro Pro Pro
1010 1015 1020

Thr Ser Arg Pro Arg Met Leu Thr Thr Pro Thr Gly Pro Glu Ser Met
1025 1030 1035 1040

Ser Thr Ser Thr Pro Ala Ile Ser Ser Pro Ser Pro Thr Thr Ala Ser
1045 1050 1055

Lys Glu Gly Asp Leu Gly Gly Lys Gln Trp Gln Asp Ser Ser Thr Gln
1060 1065 1070

Cura 468 SEQ list 0705

Pro Glu Leu Ser Ser Arg Tyr Leu Ile Ser Thr Gly Ser Thr Ser Gln
1075 1080 1085

Pro Ile Leu Thr Ser Gln Ser Leu Ser Ile Gln Pro Ser Glu Glu Asn
1090 1095 1100

Val Ser Ser Ser Asp Thr Gly Pro Thr Ser Glu Gly Gly Leu Val Ala
1105 1110 1115 1120

Thr Thr Thr Ser Gly Ser Gly Leu Ser Ser Ser Arg Asn Pro Ile Thr
1125 1130 1135

Trp Pro Val Thr Pro Phe Tyr Asn Thr Leu Thr Lys Gly Pro Glu Met
1140 1145 1150

Glu Ile His Ser Gly Ser Gly Glu Glu Arg Glu Gln Pro Glu Asp Lys
1155 1160 1165

Asp Glu Ser Asn Pro Val Ile Trp Thr Lys Ile Arg Val Pro Gly Asn
1170 1175 1180

Asp Ala Pro Val Glu Ser Thr Glu Met Pro Leu Ala Pro Pro Leu Thr
1185 1190 1195 1200

Pro Asp Leu Ser Arg Glu Ser Trp Trp Pro Pro Phe Ser Thr Val Met
1205 1210 1215

Glu Gly Leu Leu Pro Ser Gln Arg Pro Thr Thr Ser Glu Thr Gly Thr
1220 1225 1230

Pro Arg Val Glu Gly Met Val Thr Glu Lys Pro Ala Asn Thr Leu Leu
1235 1240 1245

Pro Leu Gly Gly Asp His Gln Pro Glu Pro Ser Gly Lys Thr Ala Asn
1250 1255 1260

Arg Asn His Leu Lys Leu Pro Asn Asn Met Asn Gln Thr Lys Ser Ser
1265 1270 1275 1280

Glu Pro Val Leu Thr Glu Glu Asp Ala Thr Ser Leu Ile Thr Glu Gly
1285 1290 1295

Phe Leu Leu Asn Ala Ser Asn Tyr Lys Gln Leu Thr Asn Gly His Gly
1300 1305 1310

Ser Ala His Trp Ile Val Gly Asn Trp Ser Glu Cys Ser Thr Thr Cys
1315 1320 1325

Gly Leu Gly Ala Tyr Trp Lys Arg Val Glu Cys Thr Thr Gln Met Asp
1330 1335 1340

Ser Asp Cys Ala Ala Ile Gln Arg Pro Asp Pro Ala Lys Arg Cys His
1345 1350 1355 1360

Leu Arg Pro Cys Ala Gly Trp Lys Val Gly Asn Trp Ser Lys Cys Ser
1365 1370 1375

Arg Asn Cys Ser Gly Gly Phe Lys Ile Arg Glu Ile Gln Cys Val Asp
1380 1385 1390

Ser Arg Asp His Arg Asn Leu Arg Pro Phe His Cys Gln Phe Leu Ala
1395 1400 1405

Cura 468 SEQ list 0705

Gly Ile Pro Pro Pro Leu Ser Met Ser Cys Asn Pro Glu Pro Cys Glu
1410 1415 1420
Ala Trp Gln Val Glu Pro Trp Ser Gln Cys Ser Arg Ser Cys Gly Gly
1425 1430 1435 1440
Gly Val Gln Glu Arg Gly Val Phe Cys Pro Gly Gly Leu Cys Asp Trp
1445 1450 1455
Thr Lys Arg Pro Thr Ser Thr Met Ser Cys Asn Glu His Leu Cys Cys
1460 1465 1470
His Trp Ala Thr Gly Asn Trp Asp Leu Cys Ser Thr Ser Cys Gly Gly
1475 1480 1485
Gly Phe Gln Lys Arg Ile Val Gln Cys Val Pro Ser Glu Gly Asn Lys
1490 1495 1500
Thr Glu Asp Gln Asp Gln Cys Leu Cys Asp His Lys Pro Arg Pro Pro
1505 1510 1515 1520
Glu Phe Lys Lys Cys Asn Gln Gln Ala Cys Lys Lys Ser Ala Asp Leu
1525 1530 1535
Leu Cys Thr Lys Asp Lys Leu Ser Ala Ser Phe Cys Gln Thr Leu Lys
1540 1545 1550
Ala Met Lys Lys Cys Ser Val Pro Thr Val Arg Ala Glu Cys Cys Phe
1555 1560 1565
Ser Cys Pro Gln Thr His Ile Thr His Thr Gln Arg Gln Arg Arg Gln
1570 1575 1580
Arg Leu Leu Gln Lys Ser Lys Glu Leu
1585 1590

<210> 31
<211> 1077
<212> PRT
<213> Homo sapiens

<400> 31

Arg Ser Gln Asp Glu Phe Leu Ser Ser Leu Glu Ser Tyr Glu Ile Ala
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20 25 30
Pro Pro Pro Arg Arg Gln Arg Arg Gly Thr Gly Ala Thr Ala Glu Ser
35 40 45
Arg Leu Phe Tyr Lys Val Ala Ser Pro Ser Thr His Phe Leu Leu Asn
50 55 60
Leu Thr Arg Ser Ser Arg Leu Leu Ala Gly His Val Ser Val Glu Tyr
65 70 75 80
Trp Thr Arg Glu Gly Leu Ala Trp Gln Arg Ala Ala Arg Pro His Cys
85 90 95
Leu Tyr Ala Gly His Leu Gln Gly Gln Ala Ser Ser Ser His Val Ala

Cura 468 SEQ list 0705
105 110

100

Ile Ser Thr Cys Gly Gly Leu His Gly Leu Ile Val Ala Asp Glu Glu
115 120 125
Glu Tyr Leu Ile Glu Pro Leu His Gly Gly Pro Lys Gly Ser Arg Ser
130 135 140
Pro Glu Glu Ser Gly Pro His Val Val Tyr Lys Arg Ser Ser Leu Arg
145 150 155 160
His Pro His Leu Asp Thr Ala Cys Gly Val Arg Asp Glu Lys Pro Trp
165 170 175
Lys Gly Arg Pro Trp Trp Leu Arg Thr Leu Lys Pro Pro Pro Ala Arg
180 185 190
Pro Leu Gly Asn Glu Thr Glu Arg Gly Gln Pro Gly Leu Lys Arg Ser
195 200 205
Val Ser Arg Glu Arg Tyr Val Glu Thr Leu Val Val Ala Asp Lys Met
210 215 220
Met Val Ala Tyr His Gly Arg Arg Asp Val Glu Gln Tyr Val Leu Ala
225 230 235 240
Ile Met Asn Ile Val Ala Lys Leu Phe Gln Asp Ser Ser Leu Gly Ser
245 250 255
Thr Val Asn Ile Leu Val Thr Arg Leu Ile Leu Leu Thr Glu Asp Gln
260 265 270
Pro Thr Leu Glu Ile Thr His His Ala Gly Lys Ser Leu Asp Ser Phe
275 280 285
Cys Lys Trp Gln Lys Ser Ile Val Asn His Ser Gly His Gly Asn Ala
290 295 300
Ile Pro Glu Asn Gly Val Ala Asn His Asp Thr Ala Val Leu Ile Thr
305 310 315 320
Arg Tyr Asp Ile Cys Ile Tyr Lys Asn Lys Pro Cys Gly Thr Leu Gly
325 330 335
Leu Ala Pro Val Gly Gly Met Cys Glu Arg Glu Arg Ser Cys Ser Val
340 345 350
Asn Glu Asp Ile Gly Leu Pro Gln Ala Phe Thr Ile Ala His Glu Ile
355 360 365
Gly His Thr Phe Gly Met Asn His Asp Gly Val Gly Asn Ser Cys Gly
370 375 380
Ala Arg Gly Gln Asp Pro Ala Lys Leu Met Ala Ala His Ile Thr Met
385 390 395 400
Lys Thr Asn Pro Phe Val Trp Ser Ser Cys Asn Arg Asp Tyr Ile Thr
405 410 415
Ser Phe Leu Asp Ser Gly Leu Gly Leu Cys Leu Asn Asn Arg Pro Pro
420 425 430
Arg Gln Asp Phe Val Tyr Pro Thr Val Ala Pro Gly Gln Ala Tyr Asp

Cura 468 SEQ list 0705

435 440 445
 Ala Asp Glu Gln Cys Arg Phe Gln His Gly Val Lys Ser Arg Gln Cys
 450 455 460
 Lys Tyr Gly Glu Val Cys Ser Glu Leu Trp Cys Leu Ser Lys Ser Asn
 465 470 475 480
 Arg Cys Ile Thr Asn Ser Ile Pro Ala Ala Glu Gly Thr Leu Cys Gln
 485 490 495
 Thr His Thr Ile Asp Lys Gly Trp Cys Tyr Lys Arg Val Cys Val Pro
 500 505 510
 Phe Gly Ser Arg Pro Glu Gly Val Asp Gly Ala Trp Gly Pro Trp Thr
 515 520 525
 Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Gly Val Ser Ser Ser
 530 535 540
 Ser Arg His Cys Asp Ser Pro Arg Pro Thr Ile Gly Gly Lys Tyr Cys
 545 550 555 560
 Leu Gly Glu Arg Arg Arg His Arg Ser Cys Asn Thr Asp Asp Cys Pro
 565 570 575
 Pro Gly Ser Gln Asp Phe Arg Glu Val Gln Cys Ser Glu Phe Asp Ser
 580 585 590
 Ile Pro Phe Arg Gly Lys Phe Tyr Lys Trp Lys Thr Tyr Arg Gly Gly
 595 600 605
 Gly Val Lys Ala Cys Ser Leu Thr Ser Leu Ala Glu Gly Phe Asn Phe
 610 615 620
 Tyr Thr Glu Arg Ala Ala Ala Val Val Asp Gly Thr Pro Cys Arg Pro
 625 630 635 640
 Asp Thr Val Asp Ile Cys Val Ser Gly Glu Cys Lys His Val Gly Cys
 645 650 655
 Asp Arg Val Leu Gly Ser Asp Leu Arg Glu Asp Lys Cys Arg Val Cys
 660 665 670
 Gly Gly Asp Gly Ser Ala Cys Glu Thr Ile Glu Gly Val Phe Ser Pro
 675 680 685
 Ala Ser Pro Gly Ala Gly Tyr Glu Asp Val Val Trp Ile Pro Lys Gly
 690 695 700
 Ser Val His Ile Phe Ile Gln Asp Leu Asn Leu Ser Leu Ser His Leu
 705 710 715 720
 Ala Leu Lys Gly Asp Gln Glu Ser Leu Leu Leu Glu Gly Leu Pro Gly
 725 730 735
 Thr Pro Gln Pro His Arg Leu Pro Leu Ala Gly Thr Thr Phe Gln Leu
 740 745 750
 Arg Gln Gly Pro Asp Gln Val Gln Ser Leu Glu Ala Leu Gly Pro Ile
 755 760 765
 Asn Ala Ser Leu Ile Val Met Val Leu Ala Arg Thr Glu Leu Pro Ala

Cura 468 SEQ list 0705
780

770

775

Leu Arg Tyr Arg Phe Asn Ala Pro Ile Ala Arg Asp Ser Leu Pro Pro
785 790 795 800
Tyr Ser Trp His Tyr Ala Pro Trp Thr Lys Cys Ser Ala Gln Cys Ala
805 810 815
Gly Gly Ser Gln Val Gln Ala Val Glu Cys Arg Asn Gln Leu Asp Ser
820 825 830
Ser Ala Val Ala Pro His Tyr Cys Ser Ala His Ser Lys Leu Pro Lys
835 840 845
Arg Gln Arg Ala Cys Asn Thr Glu Pro Cys Pro Pro Asp Trp Val Val
850 855 860
Gly Asn Trp Ser Leu Cys Ser Arg Ser Cys Asp Ala Gly Val Arg Ser
865 870 875 880
Arg Ser Val Val Cys Gln Arg Arg Val Ser Ala Ala Glu Glu Lys Ala
885 890 895
Leu Asp Asp Ser Ala Cys Pro Gln Pro Arg Pro Pro Val Leu Glu Ala
900 905 910
Cys His Gly Pro Thr Cys Pro Pro Glu Trp Ala Ala Leu Asp Trp Ser
915 920 925
Glu Cys Thr Pro Ser Cys Gly Pro Gly Leu Arg His Arg Val Val Leu
930 935 940
Cys Lys Ser Ala Asp His Arg Ala Thr Leu Pro Pro Ala His Cys Ser
945 950 955 960
Pro Ala Ala Lys Pro Pro Ala Thr Met Arg Cys Asn Leu Arg Arg Cys
965 970 975
Pro Pro Ala Arg Trp Val Ala Gly Glu Trp Gly Glu Cys Ser Ala Gln
980 985 990
Cys Gly Val Gly Gln Arg Gln Arg Ser Val Arg Cys Thr Ser His Thr
995 1000 1005
Gly Gln Ala Ser His Glu Cys Thr Glu Ala Leu Arg Pro Pro Thr Thr
1010 1015 1020
Gln Gln Cys Glu Ala Lys Cys Asp Ser Pro Thr Pro Gly Asp Gly Pro
1025 1030 1035 1040
Glu Glu Cys Lys Asp Val Asn Lys Val Ala Tyr Cys Pro Leu Val Leu
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Lys Phe Gln Phe Cys Ser Arg Ala Tyr Phe Arg Gln Met Cys Cys Lys
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Thr Cys Gln Gly His
1075

<210> 32
<211> 997
<212> PRT

Cura 468 SEQ list 0705

<213> Homo sapiens

<400> 32

Met Pro Gly Gly Pro Ser Pro Arg Ser Pro Ala Pro Leu Leu Arg Pro
 1 5 10 15
 Leu Leu Leu Leu Leu Cys Ala Leu Ala Pro Gly Ala Pro Gly Pro Ala
 20 25 30
 Pro Gly Arg Ala Thr Glu Gly Arg Ala Ala Leu Asp Ile Val His Pro
 35 40 45
 Val Arg Val Asp Ala Gly Gly Ser Phe Leu Ser Tyr Glu Leu Trp Pro
 50 55 60
 Arg Ala Leu Arg Lys Arg Asp Val Ser Val Arg Arg Asp Ala Pro Ala
 65 70 75 80
 Phe Tyr Glu Leu Gln Tyr Arg Gly Arg Glu Leu Arg Phe Asn Leu Thr
 85 90 95
 Ala Asn Gln His Leu Leu Ala Pro Gly Phe Val Ser Glu Thr Arg Arg
 100 105 110
 Arg Gly Gly Leu Gly Arg Ala His Ile Arg Ala His Thr Pro Ala Cys
 115 120 125
 His Leu Leu Gly Glu Val Gln Asp Pro Glu Leu Glu Gly Gly Leu Ala
 130 135 140
 Ala Ile Ser Ala Cys Asp Gly Leu Lys Gly Val Phe Gln Leu Ser Asn
 145 150 155 160
 Glu Asp Tyr Phe Ile Glu Pro Leu Asp Ser Ala Pro Ala Arg Pro Gly
 165 170 175
 His Ala Gln Pro His Val Val Tyr Lys Arg Gln Ala Pro Glu Arg Leu
 180 185 190
 Ala Gln Arg Gly Asp Ser Ser Ala Pro Ser Thr Cys Gly Val Gln Val
 195 200 205
 Tyr Pro Glu Leu Glu Ser Arg Arg Glu Arg Trp Glu Gln Arg Gln Gln
 210 215 220
 Trp Arg Arg Pro Arg Leu Arg Arg Leu His Gln Arg Ser Val Ser Lys
 225 230 235 240
 Glu Lys Trp Val Glu Thr Leu Val Val Ala Asp Ala Lys Met Val Glu
 245 250 255
 Tyr His Gly Gln Pro Gln Val Glu Ser Tyr Val Leu Thr Ile Met Asn
 260 265 270
 Met Val Ala Gly Leu Phe His Asp Pro Ser Ile Gly Asn Pro Ile His
 275 280 285
 Ile Thr Ile Val Arg Leu Val Leu Leu Glu Asp Glu Glu Glu Asp Leu
 290 295 300
 Lys Ile Thr His His Ala Asp Asn Thr Leu Lys Ser Phe Cys Lys Trp
 305 310 315 320

Cura 468 SEQ list 0705

Gln Lys Ser Ile Asn Met Lys Gly Asp Ala His Pro Leu His His Asp
325 330 335

Thr Ala Ile Leu Leu Thr Arg Lys Asp Leu Cys Ala Ala Met Asn Arg
340 345 350

Pro Cys Glu Thr Leu Gly Leu Ser His Val Ala Gly Met Cys Gln Pro
355 360 365

His Arg Ser Cys Ser Ile Asn Glu Asp Thr Gly Leu Pro Leu Ala Phe
370 375 380

Thr Val Ala His Glu Leu Gly His Ser Phe Gly Ile Gln His Asp Gly
385 390 395 400

Ser Gly Asn Asp Cys Glu Pro Val Gly Lys Arg Pro Phe Ile Met Ser
405 410 415

Pro Gln Leu Leu Tyr Asp Ala Ala Pro Leu Thr Trp Ser Arg Cys Ser
420 425 430

Arg Gln Tyr Ile Thr Arg Phe Leu Asp Arg Gly Trp Gly Leu Cys Leu
435 440 445

Asp Asp Pro Pro Ala Lys Asp Ile Ile Asp Phe Pro Ser Val Pro Pro
450 455 460

Gly Val Leu Tyr Asp Val Ser His Gln Cys Arg Leu Gln Tyr Gly Ala
465 470 475 480

Tyr Ser Ala Phe Cys Glu Asp Met Asp Asn Val Cys His Thr Leu Trp
485 490 495

Cys Ser Val Gly Thr Thr Cys His Ser Lys Leu Asp Ala Ala Val Asp
500 505 510

Gly Thr Arg Cys Gly Glu Asn Lys Trp Cys Leu Ser Gly Glu Cys Val
515 520 525

Pro Val Gly Phe Arg Pro Glu Ala Val Asp Gly Gly Trp Ser Gly Trp
530 535 540

Ser Ala Trp Ser Ile Cys Ser Arg Ser Cys Gly Met Gly Val Gln Ser
545 550 555 560

Ala Glu Arg Gln Cys Thr Gln Pro Thr Pro Lys Tyr Lys Gly Arg Tyr
565 570 575

Cys Val Gly Glu Arg Lys Arg Phe Arg Leu Cys Asn Leu Gln Ala Cys
580 585 590

Pro Ala Gly Arg Pro Ser Phe Arg His Val Gln Cys Ser His Phe Asp
595 600 605

Ala Met Leu Tyr Lys Gly Gln Leu His Thr Trp Val Pro Val Val Asn
610 615 620

Asp Val Asn Pro Cys Glu Leu His Cys Arg Pro Ala Asn Glu Tyr Phe
625 630 635 640

Ala Lys Lys Leu Arg Asp Ala Val Val Asp Gly Thr Pro Cys Tyr Gln
645 650 655

Cura 468 SEQ list 0705

Val Arg Ala Ser Arg Asp Leu Cys Ile Asn Gly Ile Cys Lys Asn Val
 660 665 670
 Gly Cys Asp Phe Glu Ile Asp Ser Gly Ala Met Glu Asp Arg Cys Gly
 675 680 685
 Val Cys His Gly Asn Gly Ser Thr Cys His Thr Val Ser Gly Thr Phe
 690 695 700
 Glu Glu Ala Glu Gly Leu Gly Tyr Val Asp Val Gly Leu Ile Pro Ala
 705 710 715 720
 Gly Ala Arg Glu Ile Arg Ile Gln Glu Val Ala Glu Ala Ala Asn Phe
 725 730 735
 Leu Ala Leu Arg Ser Glu Asp Pro Glu Lys Tyr Phe Leu Asn Gly Gly
 740 745 750
 Trp Thr Ile Gln Trp Asn Gly Asp Tyr Gln Val Ala Gly Thr Thr Phe
 755 760 765
 Thr Tyr Ala Arg Arg Gly Asn Trp Glu Asn Leu Thr Ser Pro Gly Pro
 770 775 780
 Thr Lys Glu Pro Val Trp Ile Gln Val Pro Ala Ser Arg Gly Pro Gly
 785 790 795 800
 Gly Gly Ser Arg Gly Gly Val Pro Arg Pro Ser Thr Leu His Gly Arg
 805 810 815
 Ser Arg Pro Gly Gly Val Ser Pro Gly Ser Val Thr Glu Pro Gly Ser
 820 825 830
 Glu Pro Gly Pro Pro Ala Ala Ala Ser Thr Ser Val Ser Pro Ser Leu
 835 840 845
 Lys Trp Pro Asn Leu Val Ala Ala Val His Arg Gly Gly Trp Gly Gln
 850 855 860
 Ala Pro Leu Gly Leu Gly Gly Trp Arg Arg His Leu Val Leu Met Gly
 865 870 875 880
 Pro Arg Leu Pro Thr Gln Leu Leu Phe Gln Glu Ser Asn Pro Gly Val
 885 890 895
 His Tyr Glu Tyr Thr Ile His Arg Glu Ala Gly Gly His Asp Glu Val
 900 905 910
 Pro Pro Pro Val Phe Ser Trp His Tyr Gly Pro Trp Thr Lys Cys Thr
 915 920 925
 Val Thr Cys Gly Arg Gly Glu Lys Trp Gly Arg His Ser Pro Thr Cys
 930 935 940
 Arg Gly Leu Val Ser Gly Gln Gly His Trp Leu Gln Leu Pro Ala His
 945 950 955 960
 Cys Trp Ala Thr Thr Gly Leu Glu Val Cys Phe Ser Glu Pro Gln Phe
 965 970 975
 Ser Ile Cys Glu Met Arg Leu Ala Ile Ala Leu Cys Pro Arg Pro Ala
 980 985 990

Cura 468 SEQ list 0705

Gly Arg Val His Gly
995

<210> 33
<211> 854
<212> PRT
<213> Homo sapiens

<400> 33

Met Met Val Ala Tyr His Gly Arg Arg Asp Val Glu Gln Tyr Val Leu
1 5 10 15
Ala Ile Met Asn Ile Val Ala Lys Leu Phe Gln Asp Ser Ser Leu Gly
20 25 30
Ser Thr Val Asn Ile Leu Val Thr Arg Leu Ile Leu Thr Glu Asp
35 40 45
Gln Pro Thr Leu Glu Ile Thr His His Ala Gly Lys Ser Leu Asp Ser
50 55 60
Phe Cys Lys Trp Gln Lys Ser Ile Val Asn His Ser Gly His Gly Asn
65 70 75 80
Ala Ile Pro Glu Asn Gly Val Ala Asn His Asp Thr Ala Val Leu Ile
85 90 95
Thr Arg Tyr Asp Ile Cys Ile Tyr Lys Asn Lys Pro Cys Gly Thr Leu
100 105 110
Gly Leu Ala Pro Val Gly Gly Met Cys Glu Arg Glu Arg Ser Cys Ser
115 120 125
Val Asn Glu Asp Ile Gly Leu Ala Thr Ala Phe Thr Ile Ala His Glu
130 135 140
Ile Gly His Thr Phe Gly Met Asn His Asp Gly Val Gly Asn Ser Cys
145 150 155 160
Gly Ala Arg Gly Gln Asp Pro Ala Lys Leu Met Ala Ala His Ile Thr
165 170 175
Met Lys Thr Asn Pro Phe Val Trp Ser Ser Cys Ser Arg Asp Tyr Ile
180 185 190
Thr Ser Phe Leu Asp Ser Gly Leu Gly Leu Cys Leu Asn Asn Arg Pro
195 200 205
Pro Arg Gln Asp Phe Val Tyr Pro Thr Val Ala Pro Gly Gln Ala Tyr
210 215 220
Asp Ala Asp Glu Gln Cys Arg Phe Gln His Gly Val Lys Ser Arg Gln
225 230 235 240
Cys Lys Tyr Gly Glu Val Cys Ser Glu Leu Trp Cys Leu Ser Lys Ser
245 250 255
Asn Arg Cys Ile Thr Asn Ser Ile Pro Ala Ala Glu Gly Thr Leu Cys
260 265 270
Gln Thr His Thr Ile Asp Lys Gly Trp Cys Tyr Lys Arg Val Cys Val
275 280 285

Cura 468 SEQ list 0705

Pro Phe Gly Ser Arg Pro Glu Gly Val Asp Gly Ala Trp Gly Pro Trp
290 295 300

Thr Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Gly Val Ser Ser
305 310 315 320

Ser Ser Arg His Cys Asp Ser Pro Arg Pro Thr Ile Gly Gly Lys Tyr
325 330 335

Cys Leu Gly Glu Arg Arg Arg His Arg Ser Cys Asn Thr Asp Asp Cys
340 345 350

Pro Pro Gly Ser Gln Asp Phe Arg Glu Val Gln Cys Ser Glu Phe Asp
355 360 365

Ser Ile Pro Phe Arg Gly Lys Phe Tyr Lys Trp Lys Thr Tyr Arg Gly
370 375 380

Gly Gly Val Lys Ala Cys Ser Leu Thr Cys Leu Ala Glu Gly Phe Asn
385 390 395 400

Phe Tyr Thr Glu Arg Ala Ala Ala Val Val Asp Gly Thr Pro Cys Arg
405 410 415

Pro Asp Thr Val Asp Ile Cys Val Ser Gly Glu Cys Lys His Val Gly
420 425 430

Cys Asp Arg Val Leu Gly Ser Asp Leu Arg Glu Asp Lys Cys Arg Val
435 440 445

Cys Gly Gly Asp Gly Ser Ala Cys Glu Thr Ile Glu Gly Val Phe Ser
450 455 460

Pro Ala Ser Pro Gly Ala Gly Tyr Glu Asp Val Val Trp Ile Pro Lys
465 470 475 480

Gly Ser Val His Ile Phe Ile Gln Asp Leu Asn Leu Ser Leu Ser His
485 490 495

Leu Ala Leu Lys Gly Asp Gln Glu Ser Leu Leu Leu Glu Gly Leu Pro
500 505 510

Gly Thr Pro Gln Pro His Arg Leu Pro Leu Ala Gly Thr Thr Phe Gln
515 520 525

Leu Arg Gln Gly Pro Asp Gln Val Gln Ser Leu Glu Ala Leu Gly Pro
530 535 540

Ile Asn Ala Ser Leu Ile Val Met Val Leu Ala Arg Thr Glu Leu Pro
545 550 555 560

Ala Leu Arg Tyr Arg Phe Asn Ala Pro Ile Ala Arg Asp Ser Leu Pro
565 570 575

Pro Tyr Ser Trp His Tyr Ala Pro Trp Thr Lys Cys Ser Ala Gln Cys
580 585 590

Ala Gly Gly Ser Gln Val Gln Ala Val Glu Cys Arg Asn Gln Leu Asp
595 600 605

Ser Ser Ala Val Ala Pro His Tyr Cys Ser Ala His Ser Lys Leu Pro
610 615 620

Cura 468 SEQ list 0705

Lys Arg Gln Arg Ala Cys Asn Thr Glu Pro Cys Pro Pro Asp Trp Val
 625 630 635 640
 Val Gly Asn Trp Ser Leu Cys Ser Arg Ser Cys Asp Ala Gly Val Arg
 645 650 655
 Ser Arg Ser Val Val Cys Gln Arg Arg Val Ser Ala Ala Glu Glu Lys
 660 665 670
 Ala Leu Asp Asp Ser Ala Cys Pro Gln Pro Arg Pro Pro Val Leu Glu
 675 680 685
 Ala Cys His Gly Pro Thr Cys Pro Pro Glu Trp Ala Ala Leu Asp Trp
 690 695 700
 Ser Glu Cys Thr Pro Ser Cys Gly Pro Gly Leu Arg His Arg Val Val
 705 710 715 720
 Leu Cys Lys Ser Ala Asp His Arg Ala Thr Leu Pro Pro Ala His Cys
 725 730 735
 Ser Pro Ala Ala Lys Pro Pro Ala Thr Met Arg Cys Asn Leu Arg Arg
 740 745 750
 Cys Pro Pro Ala Arg Trp Val Ala Gly Glu Trp Gly Glu Cys Ser Ala
 755 760 765
 Gln Cys Gly Val Gly Gln Arg Gln Arg Ser Val Arg Cys Thr Ser His
 770 775 780
 Thr Gly Gln Ala Ser His Glu Cys Thr Glu Ala Leu Arg Pro Pro Thr
 785 790 795 800
 Thr Gln Gln Cys Glu Ala Lys Cys Asp Ser Pro Thr Pro Gly Asp Gly
 805 810 815
 Pro Glu Glu Cys Lys Asp Val Asn Lys Val Ala Tyr Cys Pro Leu Val
 820 825 830
 Leu Lys Phe Gln Phe Cys Ser Arg Ala Tyr Phe Arg Gln Met Cys Cys
 835 840 845
 Lys Thr Cys His Gly His
 850

<210> 34
 <211> 860
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (450)
 <223> Wherein Xaa is any amino acid.

<400> 34
 Met Glu Ile Leu Trp Lys Thr Leu Thr Trp Ile Leu Ser Leu Ile Met
 1 5 10 15
 Ala Ser Ser Glu Phe His Ser Asp His Arg Leu Ser Tyr Ser Ser Gln
 20 25 30

Cura 468 SEQ list 0705

Glu Glu Phe Leu Thr Tyr Leu Glu His Tyr Gln Leu Thr Ile Pro Ile
 35 40 45
 Arg Val Asp Gln Asn Gly Ala Phe Leu Ser Phe Thr Val Lys Asn Asp
 50 55 60
 Lys His Ser Arg Arg Arg Arg Ser Met Asp Pro Ile Asp Pro Gln Gln
 65 70 75 80
 Ala Val Ser Lys Leu Phe Phe Lys Leu Ser Ala Tyr Gly Lys His Phe
 85 90 95
 His Leu Asn Leu Thr Leu Asn Thr Asp Phe Val Ser Lys His Phe Thr
 100 105 110
 Val Glu Tyr Trp Gly Lys Asp Gly Pro Gln Trp Lys His Asp Phe Leu
 115 120 125
 Asp Asn Cys His Tyr Thr Gly Tyr Leu Gln Asp Gln Arg Ser Thr Thr
 130 135 140
 Lys Val Ala Leu Ser Asn Cys Val Gly Leu His Gly Val Ile Ala Thr
 145 150 155 160
 Glu Asp Glu Glu Tyr Phe Ile Glu Pro Leu Lys Asn Thr Thr Glu Asp
 165 170 175
 Ser Lys His Phe Ser Tyr Glu Asn Gly His Pro His Val Ile Tyr Lys
 180 185 190
 Lys Ser Ala Leu Gln Gln Arg His Leu Tyr Asp His Ser His Cys Gly
 195 200 205
 Val Ser Asp Phe Thr Arg Ser Gly Lys Pro Trp Trp Leu Asn Asp Thr
 210 215 220
 Ser Thr Val Ser Tyr Ser Leu Pro Ile Asn Asn Thr His Ile His His
 225 230 235 240
 Arg Gln Lys Arg Ser Val Ser Ile Glu Arg Phe Val Glu Thr Leu Val
 245 250 255
 Val Ala Asp Lys Met Met Val Gly Tyr His Gly Arg Lys Asp Ile Glu
 260 265 270
 His Tyr Ile Leu Ser Val Met Asn Ile Val Ala Lys Leu Tyr Arg Asp
 275 280 285
 Ser Ser Leu Gly Asn Val Val Asn Ile Ile Val Ala Arg Leu Ile Val
 290 295 300
 Leu Thr Glu Asp Gln Pro Asn Leu Glu Ile Asn His His Ala Asp Lys
 305 310 315 320
 Ser Leu Asp Ser Phe Cys Lys Trp Gln Lys Ser Ile Leu Ser His Gln
 325 330 335
 Ser Asp Gly Asn Thr Ile Pro Glu Asn Gly Ile Ala His His Asp Asn
 340 345 350
 Ala Val Leu Ile Thr Arg Tyr Asp Ile Cys Thr Tyr Lys Asn Lys Pro
 355 360 365

Cura 468 SEQ list 0705

Cys Gly Thr Leu Gly Leu Ala Ser Val Ala Gly Met Cys Glu Pro Glu
 370 375 380
 Arg Ser Cys Ser Ile Asn Glu Asp Ile Gly Leu Gly Ser Ala Phe Thr
 385 390 395 400
 Ile Ala His Glu Ile Val His Asn Phe Gly Met Asn His Asp Gly Ile
 405 410 415
 Gly Asn Ser Cys Gly Arg Lys Val Met Lys Gln Gln Asn Tyr Gly Ser
 420 425 430
 Ser His Tyr Cys Glu Tyr Gln Ser Phe Phe Leu Val Cys Leu Gln Ser
 435 440 445
 Arg Xaa His His Gln Leu Phe Arg Glu Val Cys Arg Glu Leu Trp Cys
 450 455 460
 Leu Ser Lys Ser Asn Arg Cys Val Thr Asn Ser Ile Pro Ala Ala Glu
 465 470 475 480
 Gly Thr Leu Cys Gln Thr Gly Asn Ile Glu Lys Gly Trp Cys Tyr Gln
 485 490 495
 Gly Asp Cys Val Pro Phe Gly Thr Trp Pro Gln Ser Ile Asp Gly Gly
 500 505 510
 Trp Gly Pro Trp Ser Leu Trp Gly Glu Cys Ser Arg Thr Cys Gly Gly
 515 520 525
 Gly Val Ser Ser Ser Leu Arg His Cys Asp Ser Pro Ala Pro Ser Gly
 530 535 540
 Gly Gly Lys Tyr Cys Leu Gly Glu Arg Lys Arg Tyr Arg Ser Cys Asn
 545 550 555 560
 Thr Asp Pro Cys Pro Leu Gly Ser Arg Asp Phe Arg Glu Lys Gln Cys
 565 570 575
 Ala Asp Phe Asp Asn Met Pro Phe Arg Gly Lys Tyr Tyr Asn Trp Lys
 580 585 590
 Pro Tyr Thr Gly Gly Gly Val Lys Pro Cys Ala Leu Asn Cys Leu Ala
 595 600 605
 Glu Gly Tyr Asn Phe Tyr Thr Glu Arg Ala Pro Ala Val Ile Asp Gly
 610 615 620
 Thr Gln Cys Asn Ala Asp Ser Leu Asp Ile Cys Ile Asn Gly Glu Cys
 625 630 635 640
 Lys His Val Gly Cys Asp Asn Ile Leu Gly Ser Asp Ala Arg Glu Asp
 645 650 655
 Arg Cys Arg Val Cys Gly Gly Gly Gly Ser Thr Cys Asp Ala Ile Glu
 660 665 670
 Gly Phe Phe Asn Asp Ser Leu Pro Arg Gly Gly Tyr Met Glu Val Val
 675 680 685
 Gln Ile Pro Arg Gly Ser Val His Ile Glu Val Arg Glu Val Ala Met
 690 695 700

Cura 468 SEQ list 0705

Ser Lys Asn Tyr Ile Ala Leu Lys Ser Glu Gly Asp Asp Tyr Tyr Ile
705 710 715 720
Asn Gly Ala Trp Thr Ile Asp Trp Pro Arg Lys Phe Asp Val Ala Gly
725 730 735
Thr Ala Phe His Tyr Lys Arg Pro Thr Asp Glu Pro Glu Ser Leu Glu
740 745 750
Ala Leu Gly Pro Thr Ser Glu Asn Leu Ile Val Met Val Leu Leu Gln
755 760 765
Glu Gln Asn Leu Gly Ile Arg Tyr Lys Phe Asn Val Pro Ile Thr Arg
770 775 780
Thr Gly Ser Gly Asp Asn Glu Val Gly Phe Thr Trp Asn His Gln Pro
785 790 795 800
Trp Ser Glu Cys Ser Ala Thr Cys Ala Gly Gly Lys Met Pro Thr Arg
805 810 815
Gln Pro Thr Gln Arg Ala Arg Trp Arg Thr Lys His Ile Leu Ser Tyr
820 825 830
Ala Leu Cys Leu Leu Lys Lys Leu Ile Gly Asn Ile Ser Cys Arg Phe
835 840 845
Ala Ser Ser Cys Asn Leu Ala Lys Glu Thr Leu Leu
850 855 860

<210> 35
<211> 936
<212> PRT
<213> Homo sapiens

<400> 35
Arg Leu Leu Ile Tyr Ala Val Leu Pro Thr Gly Asp Val Ile Gly Asp
1 5 10 15
Ser Ala Lys Tyr Asp Val Glu Asn Cys Leu Ala Asn Lys Val Asp Leu
20 25 30
Ser Phe Ser Pro Ser Gln Ser Leu Pro Ala Ser His Ala His Leu Arg
35 40 45
Val Thr Ala Ala Pro Gln Ser Val Cys Ala Leu Arg Ala Val Asp Gln
50 55 60
Ser Val Leu Leu Met Lys Pro Asp Ala Glu Leu Ser Ala Ser Ser Val
65 70 75 80
Tyr Asn Leu Leu Pro Glu Lys Asp Leu Thr Gly Phe Pro Gly Pro Leu
85 90 95
Asn Asp Gln Asp Asn Glu Asp Cys Ile Asn Arg His Asn Val Tyr Ile
100 105 110
Asn Gly Ile Thr Tyr Thr Pro Val Ser Ser Thr Asn Glu Lys Asp Met
115 120 125
Tyr Ser Phe Leu Glu Asp Met Gly Leu Lys Ala Phe Thr Asn Ser Lys

Cura 468 SEQ list 0705
140

130

135

Ile Arg Lys Pro Lys Met Cys Pro Gln Leu Gln Gln Tyr Glu Met His
145 150 155 160
Gly Pro Glu Gly Leu Arg Val Gly Phe Tyr Glu Ser Asp Val Met Gly
165 170 175
Arg Gly His Ala Arg Leu Val His Val Glu Glu Pro His Thr Glu Thr
180 185 190
Val Arg Lys Tyr Phe Pro Glu Thr Trp Ile Trp Asp Leu Val Val Val
195 200 205
Asn Ser Ala Gly Val Ala Glu Val Gly Val Thr Val Pro Asp Thr Ile
210 215 220
Thr Glu Trp Lys Ala Gly Ala Phe Cys Leu Ser Glu Asp Ala Gly Leu
225 230 235 240
Gly Ile Ser Ser Thr Ala Ser Leu Arg Ala Phe Gln Pro Phe Phe Val
245 250 255
Glu Leu Thr Met Pro Tyr Ser Val Ile Arg Gly Glu Ala Phe Thr Leu
260 265 270
Lys Ala Thr Val Leu Asn Tyr Leu Pro Lys Cys Ile Arg Val Ser Val
275 280 285
Gln Leu Glu Ala Ser Pro Ala Phe Leu Ala Val Pro Val Glu Lys Glu
290 295 300
Gln Ala Pro His Cys Ile Cys Ala Asn Gly Arg Gln Thr Val Ser Trp
305 310 315 320
Ala Val Thr Pro Lys Ser Leu Gly Asn Val Asn Phe Thr Val Ser Ala
325 330 335
Glu Ala Leu Glu Ser Gln Glu Leu Cys Gly Thr Glu Val Pro Ser Val
340 345 350
Pro Glu His Gly Arg Lys Asp Thr Val Ile Lys Pro Leu Leu Val Glu
355 360 365
Pro Glu Gly Leu Glu Lys Glu Thr Thr Phe Asn Ser Leu Leu Cys Pro
370 375 380
Ser Gly Gly Glu Val Ser Glu Glu Leu Ser Leu Lys Leu Pro Pro Asn
385 390 395 400
Val Val Glu Glu Ser Ala Arg Ala Ser Val Ser Val Leu Gly Asp Ile
405 410 415
Leu Gly Ser Ala Met Gln Asn Thr Gln Asn Leu Leu Gln Met Pro Tyr
420 425 430
Gly Cys Gly Glu Gln Asn Met Val Leu Phe Ala Pro Asn Ile Tyr Val
435 440 445
Leu Asp Tyr Leu Asn Glu Thr Gln Gln Leu Thr Pro Glu Ile Lys Ser
450 455 460
Lys Ala Ile Gly Tyr Leu Asn Thr Gly Tyr Gln Arg Gln Leu Asn Tyr

Cura 468 SEQ list 0705
475

465 470 480
Lys His Tyr Asp Gly Ser Tyr Ser Thr Phe Gly Glu Arg Tyr Gly Arg
 485 490 495
Asn Gln Gly Asn Thr Trp Leu Thr Ala Phe Val Leu Lys Thr Phe Ala
 500 505 510
Gln Ala Arg Ala Tyr Ile Phe Ile Asp Glu Ala His Ile Thr Gln Ala
 515 520 525
Leu Ile Trp Leu Ser Gln Arg Gln Lys Asp Asn Gly Cys Phe Arg Ser
 530 535 540
Ser Gly Ser Leu Leu Asn Asn Ala Ile Lys Gly Gly Val Glu Asp Glu
545 550 555 560
Val Thr Leu Ser Ala Tyr Ile Thr Ile Ala Leu Leu Glu Ile Pro Leu
 565 570 575
Thr Val Thr His Pro Val Val Arg Asn Ala Leu Phe Cys Leu Glu Ser
 580 585 590
Ala Trp Lys Thr Ala Gln Glu Gly Asp His Gly Ser His Val Tyr Thr
 595 600 605
Lys Ala Leu Leu Ala Tyr Ala Phe Ala Leu Ala Gly Asn Gln Asp Lys
610 615 620
Arg Lys Glu Val Leu Lys Ser Leu Asn Glu Glu Ala Val Lys Lys Asp
625 630 635 640
Asn Ser Val His Trp Glu Arg Pro Gln Lys Pro Lys Ala Pro Val Gly
 645 650 655
His Phe Tyr Glu Pro Gln Ala Pro Ser Ala Glu Val Glu Met Thr Ser
 660 665 670
Tyr Val Leu Leu Ala Tyr Leu Thr Ala Gln Pro Ala Pro Thr Ser Glu
675 680 685
Asp Leu Thr Ser Ala Thr Asn Ile Val Lys Trp Ile Thr Lys Gln Gln
690 695 700
Asn Ala Gln Gly Gly Phe Ser Ser Thr Gln Asp Thr Val Val Ala Leu
705 710 715 720
His Ala Leu Ser Lys Tyr Gly Ala Ala Thr Phe Thr Arg Thr Gly Lys
 725 730 735
Ala Ala Gln Val Thr Ile Gln Ser Ser Gly Thr Phe Ser Ser Lys Phe
740 745 750
Gln Val Asp Asn Asn Asn Arg Leu Leu Leu Gln Gln Val Ser Leu Pro
755 760 765
Glu Leu Pro Gly Glu Tyr Ser Met Lys Val Thr Gly Glu Gly Cys Val
770 775 780
Tyr Leu Gln Thr Ser Leu Lys Tyr Asn Ile Leu Pro Glu Lys Glu Glu
785 790 795 800
Phe Pro Phe Ala Leu Gly Val Gln Thr Leu Pro Gln Thr Cys Asp Glu

Cura 468 SEQ list 0705

805

810

815

Pro Lys Ala His Thr Ser Phe Gln Ile Ser Leu Ser Val Ser Tyr Thr
820 825 830
Gly Ser Arg Ser Ala Ser Asn Met Ala Ile Val Asp Val Lys Met Val
835 840 845
Ser Gly Phe Ile Pro Leu Lys Pro Thr Val Lys Met Leu Glu Arg Ser
850 855 860
Asn His Val Ser Arg Thr Glu Val Ser Ser Asn His Val Leu Ile Tyr
865 870 875 880
Leu Asp Lys Val Ser Asn Gln Thr Leu Ser Leu Phe Phe Thr Val Leu
885 890 895
Gln Asp Val Pro Val Arg Asp Leu Lys Pro Ala Ile Val Lys Val Tyr
900 905 910
Asp Tyr Tyr Glu Thr Gly Glu Phe Ala Ile Ala Glu Tyr Asn Ala Pro
915 920 925
Cys Ser Lys Asp Leu Gly Asn Ala
930 935

<210> 36

<211> 898

<212> PRT

<213> Homo sapiens

<400> 36

Arg Leu Leu Ile Tyr Ala Val Leu Pro Thr Gly Asp Val Ile Gly Asp
1 5 10 15
Ser Ala Lys Tyr Asp Val Glu Asn Cys Leu Ala Asn Lys Val Asp Leu
20 25 30
Ser Phe Ser Pro Ser Gln Ser Leu Pro Ala Ser His Ala His Leu Arg
35 40 45
Val Thr Ala Ala Pro Gln Ser Val Cys Ala Leu Arg Ala Val Asp Gln
50 55 60
Ser Val Leu Leu Met Lys Pro Asp Ala Glu Leu Ser Ala Ser Ser Val
65 70 75 80
Tyr Asn Leu Leu Pro Glu Lys Asp Leu Thr Gly Phe Pro Gly Pro Leu
85 90 95
Asn Asp Gln Asp Asp Glu Asp Cys Ile Asn Arg His Asn Val Tyr Ile
100 105 110
Asn Gly Ile Thr Tyr Thr Pro Val Ser Ser Thr Asn Glu Lys Asp Met
115 120 125
Tyr Ser Phe Leu Glu Asp Met Gly Leu Lys Ala Phe Thr Asn Ser Lys
130 135 140
Ile Arg Lys Glu Glu Pro His Thr Glu Thr Val Arg Lys Tyr Phe Pro
145 150 155 160

Cura 468 SEQ list 0705

Glu Thr Trp Ile Trp Asp Leu Val Val Val Asn Ser Ala Gly Val Ala
 165 170 175
 Glu Val Gly Val Thr Val Pro Asp Thr Ile Thr Glu Trp Lys Ala Gly
 180 185 190
 Ala Phe Cys Leu Ser Glu Asp Ala Gly Leu Gly Ile Ser Ser Thr Ala
 195 200 205
 Ser Leu Arg Ala Phe Gln Pro Phe Phe Val Glu Leu Thr Met Pro Tyr
 210 215 220
 Ser Val Ile Arg Gly Glu Ala Phe Thr Leu Lys Ala Thr Val Leu Asn
 225 230 235 240
 Tyr Leu Pro Lys Cys Ile Arg Val Ser Val Gln Leu Glu Ala Ser Pro
 245 250 255
 Ala Phe Leu Ala Val Pro Val Glu Lys Glu Gln Ala Pro His Cys Ile
 260 265 270
 Cys Ala Asn Gly Arg Gln Thr Val Ser Trp Ala Val Thr Pro Lys Ser
 275 280 285
 Leu Gly Asn Val Asn Phe Thr Val Ser Ala Glu Ala Leu Glu Ser Gln
 290 295 300
 Glu Leu Cys Gly Thr Glu Val Pro Ser Val Pro Glu His Gly Arg Lys
 305 310 315 320
 Asp Thr Val Ile Lys Pro Leu Leu Val Glu Pro Glu Gly Leu Glu Lys
 325 330 335
 Glu Thr Thr Phe Asn Ser Leu Leu Cys Pro Ser Gly Gly Glu Val Ser
 340 345 350
 Glu Glu Leu Ser Leu Lys Leu Pro Pro Asn Val Val Glu Glu Ser Ala
 355 360 365
 Arg Ala Ser Val Ser Val Leu Gly Asp Ile Leu Gly Ser Ala Met Gln
 370 375 380
 Asn Thr Gln Asn Leu Leu Gln Met Pro Tyr Gly Cys Gly Glu Gln Asn
 385 390 395 400
 Met Val Leu Phe Ala Pro Asn Ile Tyr Val Leu Asp Tyr Leu Asn Glu
 405 410 415
 Thr Gln Gln Leu Thr Pro Glu Val Lys Ser Lys Ala Ile Gly Tyr Leu
 420 425 430
 Asn Thr Gly Tyr Gln Arg Gln Leu Asn Tyr Lys His Tyr Asp Gly Ser
 435 440 445
 Tyr Ser Thr Phe Gly Glu Arg Tyr Gly Arg Asn Gln Gly Asn Thr Trp
 450 455 460
 Leu Thr Ala Phe Val Leu Lys Thr Phe Ala Gln Ala Arg Ala Tyr Ile
 465 470 475 480
 Phe Ile Asp Glu Ala His Ile Thr Gln Ala Leu Ile Trp Leu Ser Gln
 485 490 495

Cura 468 SEQ list 0705

Arg Gln Lys Asp Asn Gly Cys Phe Arg Ser Ser Gly Ser Leu Leu Asn
 500 505 510
 Asn Ala Ile Lys Gly Gly Val Glu Asp Glu Val Thr Leu Ser Ala Tyr
 515 520 525
 Ile Thr Ile Ala Leu Leu Glu Ile Pro Leu Thr Val Thr His Pro Val
 530 535 540
 Val Arg Asn Ala Leu Phe Cys Leu Glu Ser Ala Trp Lys Thr Ala Gln
 545 550 555 560
 Glu Gly Asp His Gly Ser His Val Tyr Thr Lys Ala Leu Leu Ala Tyr
 565 570 575
 Ala Phe Ala Leu Ala Gly Asn Gln Asp Lys Arg Lys Glu Val Leu Lys
 580 585 590
 Ser Leu Asn Glu Glu Ala Val Lys Lys Asp Asn Ser Val His Trp Glu
 595 600 605
 Arg Pro Gln Lys Pro Lys Ala Pro Val Gly His Phe Tyr Glu Pro Gln
 610 615 620
 Ala Pro Ser Ala Glu Val Glu Met Thr Ser Tyr Val Leu Leu Ala Tyr
 625 630 635 640
 Leu Thr Ala Gln Pro Ala Pro Thr Ser Glu Asp Leu Thr Ser Ala Thr
 645 650 655
 Asn Ile Val Lys Trp Ile Thr Lys Gln Gln Asn Ala Gln Gly Gly Phe
 660 665 670
 Ser Ser Thr Gln Asp Thr Val Val Ala Leu His Ala Leu Ser Lys Tyr
 675 680 685
 Gly Ala Ala Thr Phe Thr Arg Thr Gly Lys Ala Ala Gln Val Thr Ile
 690 695 700
 Gln Ser Ser Gly Thr Phe Ser Ser Lys Phe Gln Val Asp Asn Asn Asn
 705 710 715 720
 Arg Leu Leu Leu Gln Gln Val Ser Leu Pro Glu Leu Pro Gly Glu Tyr
 725 730 735
 Ser Met Lys Val Thr Gly Glu Gly Cys Val Tyr Leu Gln Thr Ser Leu
 740 745 750
 Lys Tyr Asn Ile Leu Pro Glu Lys Glu Glu Phe Pro Phe Ala Leu Gly
 755 760 765
 Val Gln Thr Leu Pro Gln Thr Cys Asp Glu Pro Lys Ala His Thr Ser
 770 775 780
 Phe Gln Ile Ser Leu Ser Val Ser Tyr Thr Gly Ser Arg Ser Ala Ser
 785 790 795 800
 Asn Met Ala Ile Val Asp Val Lys Met Val Ser Gly Phe Ile Pro Leu
 805 810 815
 Lys Pro Thr Val Lys Met Leu Glu Arg Ser Asn His Val Ser Arg Thr
 820 825 830

Cura 468 SEQ list 0705

Glu Val Ser Ser Asn His Val Leu Ile Tyr Leu Asp Lys Val Ser Asn
835 840 845
Gln Thr Leu Ser Leu Phe Phe Thr Val Leu Gln Asp Val Pro Val Arg
850 855 860
Asp Leu Lys Pro Ala Ile Val Lys Val Tyr Asp Tyr Tyr Glu Thr Asp
865 870 875 880
Glu Phe Ala Ile Ala Glu Tyr Asn Ala Pro Cys Ser Lys Asp Leu Gly
885 890 895
Asn Ala

<210> 37
<211> 936
<212> PRT
<213> Homo sapiens

<400> 37
Arg Leu Leu Ile Tyr Ala Val Leu Pro Thr Gly Asp Val Ile Gly Asp
1 5 10 15
Ser Ala Lys Tyr Asp Val Glu Asn Glu Leu Ala Asn Lys Val Asp Leu
20 25 30
Ser Phe Ser Pro Ser Gln Ser Leu Pro Ala Ser His Ala His Leu Arg
35 40 45
Val Thr Ala Ala Pro Gln Ser Val Cys Ala Leu Arg Ala Val Asp Gln
50 55 60
Ser Val Leu Leu Met Lys Pro Asp Ala Glu Leu Ser Ala Ser Ser Val
65 70 75 80
Tyr Asn Leu Leu Pro Glu Lys Asp Leu Thr Gly Phe Pro Gly Pro Leu
85 90 95
Asn Asp Gln Asp Asp Glu Asp Cys Ile Asn Arg His Asn Val Tyr Ile
100 105 110
Asn Gly Ile Thr Tyr Thr Pro Val Ser Ser Thr Asn Glu Lys Asp Met
115 120 125
Tyr Ser Phe Leu Glu Asp Met Gly Leu Lys Ala Phe Thr Asn Ser Lys
130 135 140
Ile Arg Lys Pro Lys Met Cys Pro Gln Leu Gln Gln Tyr Glu Met His
145 150 155 160
Gly Pro Glu Gly Leu Arg Val Gly Phe Tyr Glu Ser Asp Val Met Gly
165 170 175
Arg Gly His Ala Arg Leu Val His Val Glu Glu Pro His Thr Glu Thr
180 185 190
Val Arg Lys Tyr Phe Pro Glu Thr Trp Ile Trp Asp Leu Val Val Val
195 200 205
Asn Ser Ala Gly Val Ala Glu Val Gly Val Thr Val Pro Asp Thr Ile
210 215 220

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Thr Glu Trp Lys Ala Gly Ala Phe Cys Leu Ser Glu Asp Ala Gly Leu
 225 230 235 240
 Gly Ile Ser Ser Thr Ala Ser Leu Arg Ala Phe Gln Pro Phe Phe Val
 245 250 255
 Glu Leu Thr Met Pro Tyr Ser Val Ile Arg Gly Glu Ala Phe Thr Leu
 260 265 270
 Lys Ala Thr Val Leu Asn Tyr Leu Pro Lys Cys Ile Arg Val Ser Val
 275 280 285
 Gln Leu Glu Ala Ser Pro Ala Phe Leu Ala Val Pro Val Glu Lys Glu
 290 295 300
 Gln Ala Pro His Cys Ile Cys Ala Asn Gly Arg Gln Thr Val Ser Trp
 305 310 315 320
 Ala Val Thr Pro Lys Ser Leu Gly Asn Val Asn Phe Thr Val Ser Ala
 325 330 335
 Glu Ala Leu Glu Ser Gln Glu Leu Cys Gly Thr Glu Val Pro Ser Val
 340 345 350
 Pro Glu His Gly Arg Lys Asp Thr Val Ile Lys Pro Leu Leu Val Glu
 355 360 365
 Pro Glu Gly Leu Glu Lys Glu Thr Thr Phe Asn Ser Leu Leu Cys Pro
 370 375 380
 Ser Gly Gly Glu Val Ser Glu Glu Leu Ser Leu Lys Leu Pro Pro Asn
 385 390 395 400
 Val Val Glu Glu Ser Ala Arg Ala Ser Val Ser Val Leu Gly Asp Ile
 405 410 415
 Leu Gly Ser Ala Met Gln Asn Thr Gln Asn Leu Leu Gln Met Pro Tyr
 420 425 430
 Gly Cys Gly Glu Glx Asn Met Val Leu Phe Ala Pro Asn Ile Tyr Val
 435 440 445
 Leu Asp Tyr Leu Asn Glu Thr Gln Gln Leu Thr Pro Glu Ile Lys Ser
 450 455 460
 Lys Ala Ile Gly Tyr Leu Asn Thr Gly Tyr Gln Arg Gln Leu Asn Tyr
 465 470 475 480
 Lys His Tyr Asp Gly Ser Tyr Ser Thr Phe Gly Glu Arg Tyr Gly Arg
 485 490 495
 Asn Gln Gly Asn Thr Trp Leu Thr Ala Phe Val Leu Lys Thr Phe Ala
 500 505 510
 Gln Ala Arg Ala Tyr Ile Phe Ile Asp Glu Ala His Ile Thr Gln Ala
 515 520 525
 Leu Ile Trp Leu Ser Gln Arg Gln Lys Asp Asn Gly Cys Phe Arg Ser
 530 535 540
 Ser Gly Ser Leu Leu Asn Asn Ala Ile Lys Gly Gly Val Glu Asp Glu
 545 550 555 560

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Val Thr Leu Ser Ala Tyr Ile Lys Ile Ala Leu Leu Glu Ile Pro Leu
 565 570 575
 Thr Val Thr His Pro Val Val Arg Asn Ala Leu Phe Cys Leu Glu Ser
 580 585 590
 Ala Trp Lys Thr Ala Glu Glu Gly Asp His Gly Ser His Val Tyr Thr
 595 600 605
 Lys Ala Leu Leu Ala Tyr Ala Phe Ala Leu Ala Gly Asn Gln Asp Lys
 610 615 620
 Arg Lys Glu Val Leu Lys Ser Leu Asn Glu Glu Ala Val Lys Lys Asp
 625 630 635 640
 Asn Ser Val His Trp Glu Arg Pro Gln Lys Pro Lys Ala Pro Val Gly
 645 650 655
 His Phe Tyr Glu Pro Gln Ala Pro Ser Ala Glu Val Glu Met Thr Ser
 660 665 670
 Tyr Val Leu Leu Ala Tyr Leu Thr Ala Gln Pro Ala Pro Thr Ser Glu
 675 680 685
 Asp Leu Thr Ser Ala Thr Asn Ile Val Lys Trp Ile Thr Lys Gln Gln
 690 695 700
 Asn Ala Gln Gly Gly Phe Ser Ser Thr Gln Asp Lys Val Val Ala Leu
 705 710 715 720
 His Ala Leu Ser Lys Tyr Gly Ala Ala Thr Phe Thr Arg Thr Gly Lys
 725 730 735
 Ala Ala Gln Val Thr Ile Gln Ser Ser Gly Thr Phe Ser Ser Lys Phe
 740 745 750
 Gln Val Asp Asn Asn Asn Arg Leu Leu Leu Gln Gln Val Ser Leu Pro
 755 760 765
 Glu Leu Pro Gly Glu Tyr Ser Met Lys Val Thr Gly Glu Gly Cys Val
 770 775 780
 Tyr Leu Gln Thr Ser Leu Lys Tyr Asn Ile Leu Pro Glu Lys Glu Glu
 785 790 795 800
 Phe Pro Phe Ala Leu Gly Val Gln Thr Leu Pro Gln Thr Cys Asp Glu
 805 810 815
 Pro Lys Ala His Thr Ser Phe Gln Ile Ser Leu Ser Val Ser Tyr Thr
 820 825 830
 Gly Ser Arg Ser Ala Ser Asn Met Ala Ile Val Asp Val Lys Met Val
 835 840 845
 Ser Gly Phe Ile Pro Leu Lys Pro Thr Val Lys Met Leu Glu Arg Ser
 850 855 860
 Asn His Val Ser Arg Thr Glu Val Ser Ser Asn His Val Leu Ile Tyr
 865 870 875 880
 Leu Asp Lys Val Ser Asn Gln Thr Leu Ser Leu Phe Phe Thr Val Leu
 885 890 895

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Gln Asp Val Pro Val Arg Asp Leu Lys Pro Ala Ile Val Lys Val Tyr
 900 905 910
 Asp Tyr Tyr Glu Thr Asp Glu Phe Ala Ile Ala Glu Tyr Asn Ala Pro
 915 920 925
 Cys Ser Lys Asp Leu Gly Asn Ala
 930 935

<210> 38
 <211> 931
 <212> PRT
 <213> Rattus norvegicus

<400> 38
 Arg Leu Val Leu Tyr Ala Ile Leu Pro Asn Gly Glu Val Val Gly Asp
 1 5 10 15
 Thr Ala Lys Tyr Glu Ile Glu Asn Cys Leu Ala Asn Lys Val Asp Leu
 20 25 30
 Val Phe Arg Pro Asn Ser Gly Leu Pro Ala Thr Arg Ala Leu Leu Ser
 35 40 45
 Val Met Ala Ser Pro Gln Ser Leu Cys Gly Leu Arg Ala Val Asp Gln
 50 55 60
 Ser Val Leu Leu Met Lys Pro Glu Thr Glu Leu Ser Ala Ser Leu Ile
 65 70 75 80
 Tyr Asp Leu Leu Pro Val Lys Asp Leu Thr Gly Phe Pro Gln Gly Ala
 85 90 95
 Asp Gln Arg Glu Glu Asp Thr Asn Gly Cys Val Lys Gln Asn Asp Thr
 100 105 110
 Tyr Ile Asn Gly Ile Leu Tyr Ser Pro Val Gln Asn Thr Asn Glu Glu
 115 120 125
 Asp Met Tyr Gly Phe Leu Lys Asp Met Gly Leu Lys Val Phe Thr Asn
 130 135 140
 Ser Asn Ile Arg Lys Pro Lys Val Cys Glu Arg Leu Arg Asp Asn Lys
 145 150 155 160
 Gly Ile Pro Ala Ala Tyr His Leu Val Ser Gln Ser His Met Asp Ala
 165 170 175
 Phe Leu Glu Ser Ser Glu Ser Pro Thr Glu Thr Arg Arg Ser Tyr Phe
 180 185 190
 Pro Glu Thr Trp Ile Trp Asp Leu Val Val Val Asp Ser Ala Gly Val
 195 200 205
 Ala Glu Val Glu Val Thr Val Pro Asp Thr Ile Thr Glu Trp Lys Ala
 210 215 220
 Gly Ala Phe Cys Leu Ser Asn Asp Thr Gly Leu Gly Leu Ser Pro Val
 225 230 235 240
 Val Gln Phe Gln Ala Phe Gln Pro Phe Phe Val Glu Leu Thr Met Pro

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245

250

255

Tyr Ser Val Ile Arg Gly Glu Ala Phe Thr Leu Lys Ala Thr Val Leu
 260 265 270
 Asn Tyr Leu Pro Thr Cys Ile Arg Val Ala Val Gln Leu Glu Ala Ser
 275 280 285
 Pro Asp Phe Leu Ala Ala Pro Glu Glu Lys Glu Gln Arg Ser His Cys
 290 295 300
 Ile Cys Met Asn Gln Arg His Thr Ala Ser Trp Ala Val Ile Pro Lys
 305 310 315 320
 Ser Leu Gly Asn Val Asn Phe Thr Val Ser Ala Glu Ala Leu Asn Ser
 325 330 335
 Lys Glu Leu Cys Gly Asn Glu Val Pro Val Val Pro Glu Gln Gly Lys
 340 345 350
 Lys Asp Thr Ile Ile Lys Ser Leu Leu Val Glu Pro Glu Gly Leu Glu
 355 360 365
 Asn Glu Val Thr Phe Asn Ser Leu Leu Cys Pro Met Gly Ala Glu Val
 370 375 380
 Ser Glu Leu Ile Ala Leu Lys Leu Pro Ser Asp Val Val Glu Glu Ser
 385 390 395 400
 Ala Arg Ala Ser Val Thr Val Leu Gly Asp Ile Leu Gly Ser Ala Met
 405 410 415
 Gln Asn Thr Gln Asp Leu Leu Lys Met Pro Tyr Gly Cys Gly Glu Gln
 420 425 430
 Asn Met Val Leu Phe Ala Pro Asn Ile Tyr Val Leu Asp Tyr Leu Asn
 435 440 445
 Glu Thr Gln Gln Leu Thr Gln Glu Ile Lys Thr Lys Ala Ile Ala Tyr
 450 455 460
 Leu Asn Thr Gly Tyr Gln Arg Gln Leu Asn Tyr Lys His Arg Asp Gly
 465 470 475 480
 Ser Tyr Ser Ala Phe Gly Asp Lys Pro Gly Arg Asn His Ala Asn Thr
 485 490 495
 Trp Leu Thr Ala Phe Val Leu Lys Ser Phe Ala Gln Ala Arg Lys Tyr
 500 505 510
 Ile Phe Ile Asp Glu Val His Ile Thr Gln Ala Leu Leu Trp Leu Ser
 515 520 525
 Gln Gln Gln Lys Asp Asn Gly Cys Phe Arg Ser Ser Gly Ser Leu Leu
 530 535 540
 Asn Asn Ala Met Lys Gly Gly Val Glu Asp Glu Val Thr Leu Ser Ala
 545 550 555 560
 Tyr Ile Thr Ile Ala Leu Leu Glu Met Ser Leu Pro Val Thr His Pro
 565 570 575
 Val Val Arg Asn Ala Leu Phe Cys Leu Asp Thr Ala Trp Lys Ser Ala

Cura 468 SEQ list 0705
585 590

580
Arg Gly Gly Ala Gly Gly Ser His Val Tyr Thr Lys Ala Leu Leu Ala
595 600 605
Tyr Ala Phe Ala Leu Ala Gly Pro Val Val Arg Asn Ala Leu Phe Cys
610 615 620
Leu Asp Thr Ala Trp Lys Ser Ala Arg Gly Gly Ala Gly Gly Ser His
625 630 635 640
Val Tyr Thr Lys Ala Leu Leu Ala Tyr Ala Phe Ala Leu Ala Gly Pro
645 650 655
Gln Ala Thr Ser Ala Glu Val Glu Met Thr Ala Tyr Val Leu Leu Ala
660 665 670
Tyr Leu Thr Thr Glu Pro Ala Pro Thr Gln Glu Asp Leu Thr Ala Ala
675 680 685
Met Leu Ile Val Lys Trp Leu Thr Lys Gln Gln Asn Ser His Gly Gly
690 695 700
Phe Ser Ser Thr Gln Asp Thr Val Val Ala Leu His Ala Leu Ser Lys
705 710 715 720
Tyr Gly Ser Ala Thr Phe Thr Arg Ala Lys Lys Ala Ala Gln Val Thr
725 730 735
Ile Arg Ser Ser Gly Thr Phe Ser Thr Lys Phe Gln Val Asn Asn Asn
740 745 750
Asn Gln Leu Leu Leu Gln Arg Val Thr Leu Pro Thr Val Pro Gly Asp
755 760 765
Tyr Thr Val Lys Val Thr Gly Glu Gly Cys Val Tyr Leu Gln Thr Ser
770 775 780
Leu Lys Tyr Ser Val Leu Pro Arg Glu Glu Glu Phe Pro Phe Ala Val
785 790 795 800
Val Val Gln Thr Leu Pro Gly Thr Cys Glu Asp Pro Lys Ala His Thr
805 810 815
Ser Phe Gln Ile Ser Leu Asn Ile Ser Tyr Thr Gly Ser Arg Ser Glu
820 825 830
Ser Asn Met Ala Ile Ala Asp Val Lys Met Val Ser Gly Phe Ile Pro
835 840 845
Leu Lys Pro Thr Val Lys Met Leu Glu Arg Ser Val His Val Ser Arg
850 855 860
Thr Glu Val Ser Asn Asn His Val Leu Ile Tyr Leu Asp Lys Val Ser
865 870 875 880
Asn Gln Thr Val Asn Leu Ser Phe Thr Val Gln Gln Asp Ile Pro Ile
885 890 895
Arg Asp Leu Lys Pro Ala Val Val Lys Val Tyr Asp Tyr Tyr Glu Lys
900 905 910
Asp Glu Phe Ala Val Ala Lys Tyr Ser Ala Pro Cys Ser Thr Asp Tyr

915

920

925

Gly Asn Ala
930

<210> 39

<211> 941

<212> PRT

<213> Cavia porcellus

<400> 39

Arg Val Leu Ile Tyr Ala Ile Leu Pro Ser Gly Glu Ile Ile Ala Asp
1 5 10 15Ser Ala Lys Tyr Asn Val Glu Asn Cys Leu Asp Asn Lys Val Asn Leu
20 25 30Ser Phe Ser Glu Gly Gln Ser Leu Pro Ala Ser Lys Thr His Leu Arg
35 40 45Val Thr Ala Ser Pro Gln Ser Leu Cys Ala Leu Arg Ala Val Asp Gln
50 55 60Ser Val Leu Leu Arg Lys Pro Glu Ala Val Leu Ser Ala Ser Ser Val
65 70 75 80Tyr Ala Leu Leu Pro Val Lys Asp Leu Thr Gly Phe Pro Gly Leu Leu
85 90 95Gly Gln Gln Glu Glu Asn Asp Gly Glu Cys Val Ser Leu Tyr Asn Thr
100 105 110Tyr Ile Asp Gly Ile Leu Tyr Ser Pro Glu Pro Asn Ile Asn Glu Lys
115 120 125Asp Met Tyr Gly Phe Leu Lys Asp Met Gly Leu Lys Val Phe Thr Asn
130 135 140Thr Lys Ile Gln Lys Pro Gln Leu Cys Ala His Val Gln Lys Phe Glu
145 150 155 160Val Pro Thr Met Ala Tyr Ser Tyr Ser Glu Ser Ser Ser Phe Arg Ser
165 170 175Gly Pro Arg Arg Val Pro Ala Val Gly Ile Ala Ala Thr Tyr Ser Glu
180 185 190Pro Pro Lys Glu Thr Val Arg Thr Tyr Ser Pro Glu Thr Trp Ile Trp
195 200 205Asp Leu Lys Val Thr Asp Ser Ser Gly Val Ala Glu Val Glu Val Thr
210 215 220Val Pro Asp Thr Ile Thr Glu Trp Lys Ala Gly Ala Phe Cys Leu Ser
225 230 235 240Asn Asp Thr Gly Leu Gly Leu Ser Pro Thr Ala Ser Leu Arg Ala Phe
245 250 255Gln Pro Phe Phe Val Glu Leu Thr Met Pro Tyr Ser Val Ile Arg Gly
260 265 270

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Glu Ala Phe Thr Leu Lys Ala Thr Val Leu Asn Tyr Leu Pro Asp Cys
275 280 285

Ile Arg Ile Ser Val His Leu Glu Ala Ser Pro Lys Phe Leu Ala Glu
290 295 300

Pro Lys Ala Lys Glu Gln Glu Ser Tyr Cys Val Cys Gly Asn Glu Arg
305 310 315 320

Gln Thr Val Ser Trp Val Val Thr Pro Lys Ser Leu Gly Asn Val Asn
325 330 335

Phe Thr Val Ser Ala Glu Ala Leu Glu Ser Ser Glu Leu Cys Gly Asn
340 345 350

Glu Lys Thr Val Val Pro Thr Tyr Gly Lys Lys Asp Thr Ile Ile Lys
355 360 365

Pro Leu Leu Val Glu Pro Glu Gly Ile Glu Lys Glu Glu Thr Trp Thr
370 375 380

Ser Leu Ile Arg Val Ser Asp Thr Thr Val Ser Glu Lys Leu His Leu
385 390 395 400

Glu Leu Pro Ser Asn Val Ile Gln Asp Ser Ala Arg Ala Thr Val Ser
405 410 415

Ile Leu Gly Asp Ile Leu Gly Ser Ala Met Gln Asn Ile Gln Asn Leu
420 425 430

Leu Gln Met Pro Tyr Gly Cys Gly Glu Gln Asn Met Val Leu Phe Ala
435 440 445

Pro Asn Ile Tyr Val Leu Asp Tyr Leu Asn Glu Thr Gln Gln Leu Thr
450 455 460

Pro Asp Ile Lys Ser Lys Ala Ile Ser Tyr Leu Ser Thr Gly Tyr Gln
465 470 475 480

Arg Gln Leu Asn Tyr Lys His Arg Asp Gly Ser Tyr Ser Thr Phe Gly
485 490 495

Glu Asn Tyr Arg Gly Gly Gln Gly Asn Thr Trp Leu Thr Ala Phe Val
500 505 510

Leu Lys Thr Phe Ser Gln Ala Arg Lys Tyr Ile Phe Ile Asp Glu Ala
515 520 525

His Ile Thr Gln Ala Leu Ser Trp Leu Ser Gln Lys Gln Lys Asp Asn
530 535 540

Gly Cys Phe Trp Ser Ser Gly Ser Leu Leu Asn Asn Ala Ile Lys Gly
545 550 555 560

Gly Val Glu Asp Glu Ile Ser Leu Ser Ala Tyr Ile Thr Ile Ala Leu
565 570 575

Leu Glu Met Ser Leu Pro Asp Thr His Pro Val Val Arg Asn Ala Leu
580 585 590

Phe Cys Leu Glu Ser Ala Trp Lys Ser Ala Lys Glu Gly Thr His Gly
595 600 605

Cura 468 SEQ list 0705

Ser His Val Tyr Thr Lys Ala Leu Leu Ala Tyr Ala Phe Ala Leu Ala
610 615 620

Gly Asn Gln Glu Arg Lys Lys Glu Ile Leu Lys Ser Leu Glu Asp Glu
625 630 635 640

Gly Val Lys Glu Asp Asn Ser Leu His Trp Ala Arg Pro Gln Lys Pro
645 650 655

Lys Val Ser Glu Gly Phe Leu Phe Lys Ser Gln Ala Pro Ser Ala Glu
660 665 670

Val Glu Met Thr Ser Tyr Val Leu Leu Ala Tyr Leu Thr Ala Arg Pro
675 680 685

Ala Pro Thr Pro Glu Asp Leu Thr Ser Ala Thr Asp Ile Val Asn Trp
690 695 700

Val Thr Lys Gln Gln Asn Ser His Gly Gly Tyr Ser Ser Thr Gln Asp
705 710 715 720

Thr Val Val Ala Leu His Ala Leu Ser Lys Tyr Ala Ala Ala Thr Phe
725 730 735

Thr Arg Thr Glu Lys Ala Ala Gln Val Thr Ile Lys Ser Ser Gly Thr
740 745 750

Phe Ser Thr Asn Phe Glu Val Asn His Asn Asn Arg Leu Leu Leu Gln
755 760 765

Gln Val Ser Leu Pro Thr Val Ser Asp Ser Tyr Thr Ile Thr Val Thr
770 775 780

Gly Glu Gly Asn Val Tyr Leu Gln Thr Ser Leu Lys Tyr Asn Val Pro
785 790 795 800

Ser Glu Lys Gly Thr Phe Pro Phe Ala Leu Glu Ala Glu Thr Val Pro
805 810 815

Gln Ala Cys Asp Gly Pro Lys Ala His Thr Ser Phe Gln Ile Ser Leu
820 825 830

Asn Val Ser Tyr Ile Gly Ser Arg Pro Val Ser Asn Met Ala Ile Val
835 840 845

Asp Val Lys Met Val Ser Gly Phe Ile Pro Leu Lys Pro Thr Val Lys
850 855 860

Asn Leu Glu Lys Ser Glu His Ile Ser Arg Thr Glu Val Ser Asn Asn
865 870 875 880

His Val Leu Ile Tyr Leu Asp Lys Val Ser Asn Gln Thr Leu Ser Leu
885 890 895

Ser Phe Phe Val Val Gln Asp Ile Glu Val Arg Asp Leu Lys Pro Ala
900 905 910

Ile Ile Lys Val Tyr Asp Tyr Tyr Glu Thr Asn Glu Phe Ala Ile Ala
915 920 925

Glu Tyr His Ala Pro Cys Ser Lys Asp Pro Gly Asn Ala
930 935 940

Cura 468 SEQ list 0705

<210> 40

<211> 373

<212> PRT

<213> Mus musculus

<400> 40

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Met Ser Thr Asp Cys Ala Gly Asn Ser Thr Cys Pro Val Asn Ser Thr
 1          5          10          15
Glu Glu Asp Pro Pro Val Gly Met Glu Gly His Ala Asn Leu Lys Leu
          20          25          30
Leu Phe Thr Val Leu Ser Ala Val Met Val Gly Leu Val Met Phe Ser
          35          40          45
Phe Gly Cys Ser Val Glu Ser Gln Lys Leu Trp Leu His Leu Arg Arg
          50          55          60
Pro Trp Gly Ile Ala Val Gly Leu Leu Ser Gln Phe Gly Leu Met Pro
          65          70          75          80
Leu Thr Ala Tyr Leu Leu Ala Ile Gly Phe Gly Leu Lys Pro Phe Gln
          85          90          95
Ala Ile Ala Val Leu Met Met Gly Ser Cys Pro Gly Gly Thr Ile Ser
          100          105          110
Asn Val Leu Thr Phe Trp Val Asp Gly Asp Met Asp Leu Ser Ile Ser
          115          120          125
Met Thr Thr Cys Ser Thr Val Ala Ala Leu Gly Met Met Pro Leu Cys
          130          135          140
Leu Tyr Ile Tyr Thr Arg Ser Trp Thr Leu Thr Gln Asn Leu Val Ile
          145          150          155          160
Pro Tyr Gln Ser Ile Gly Ile Thr Leu Val Ser Leu Val Val Pro Val
          165          170          175
Ala Ser Gly Val Tyr Val Asn Tyr Arg Trp Pro Lys Gln Ala Thr Val
          180          185          190
Ile Leu Lys Val Gly Ala Ile Leu Gly Gly Met Leu Leu Leu Val Val
          195          200          205
Ala Val Thr Gly Met Val Leu Ala Lys Gly Trp Asn Thr Asp Val Thr
          210          215          220
Leu Leu Val Ile Ser Cys Ile Phe Pro Leu Val Gly His Val Thr Gly
          225          230          235          240
Phe Leu Leu Ala Phe Leu Thr His Gln Ser Trp Gln Arg Cys Arg Thr
          245          250          255
Ile Ser Ile Glu Thr Gly Ala Gln Asn Ile Gln Leu Cys Ile Ala Met
          260          265          270
Leu Gln Leu Ser Phe Ser Ala Glu Tyr Leu Val Gln Leu Leu Asn Phe
          275          280          285
Ala Leu Ala Tyr Gly Leu Phe Gln Val Leu His Gly Leu Leu Ile Val
          290          295          300

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Cura 468 SEQ list 0705

Ala Ala Tyr Gln Ala Tyr Lys Arg Arg Gln Lys Ser Lys Cys Arg Arg
 305 310 315 320
 Gln His Pro Asp Cys Pro Asp Val Cys Tyr Glu Lys Gln Pro Arg Glu
 325 330 335
 Thr Ser Ala Phe Leu Asp Lys Gly Asp Glu Ala Ala Val Thr Leu Gly
 340 345 350
 Pro Val Gln Pro Glu Gln His His Arg Ala Ala Glu Leu Thr Ser His
 355 360 365
 Ile Pro Ser Cys Glu
 370

<210> 41

<211> 347

<212> PRT

<213> Oryzctolagus cuniculus

<400> 41

Met Ser Asn Leu Thr Val Gly Cys Leu Ala Asn Ala Thr Val Cys Glu
 1 5 10 15
 Gly Ala Ser Cys Val Ala Pro Glu Ser Asn Phe Asn Ala Ile Leu Ser
 20 25 30
 Val Val Leu Ser Thr Val Leu Thr Ile Leu Leu Ala Leu Val Met Phe
 35 40 45
 Ser Met Gly Cys Asn Val Glu Ile Lys Lys Phe Leu Gly His Ile Arg
 50 55 60
 Arg Pro Trp Gly Ile Phe Ile Gly Phe Leu Cys Gln Phe Gly Ile Met
 65 70 75 80
 Pro Leu Thr Gly Phe Val Leu Ala Val Ala Phe Gly Ile Met Pro Ile
 85 90 95
 Gln Ala Val Val Val Leu Ile Met Gly Cys Cys Pro Gly Gly Thr Ala
 100 105 110
 Ser Asn Ile Leu Ala Tyr Trp Val Asp Gly Asp Met Asp Leu Ser Val
 115 120 125
 Ser Met Thr Thr Cys Ser Thr Leu Leu Ala Leu Gly Met Met Pro Leu
 130 135 140
 Cys Leu Tyr Val Tyr Thr Lys Met Trp Val Asp Ser Gly Thr Ile Val
 145 150 155 160
 Ile Pro Tyr Asp Asn Ile Gly Thr Ser Leu Val Ala Leu Val Val Pro
 165 170 175
 Val Ser Ile Gly Met Phe Val Asn His Lys Trp Pro Gln Lys Ala Lys
 180 185 190
 Ile Ile Leu Lys Val Gly Ser Ile Ala Gly Ala Val Leu Ile Val Leu
 195 200 205
 Ile Ala Val Val Gly Gly Ile Leu Tyr Gln Ser Ala Trp Ile Ile Glu

Cura 468 SEQ list 0705
220

210

215

Pro Lys Leu Trp Ile Ile Gly Thr Ile Phe Pro Met Ala Gly Tyr Ser
225 230 235 240
Leu Gly Phe Phe Leu Ala Arg Ile Ala Gly Gln Pro Trp Tyr Arg Cys
245 250 255
Arg Thr Val Ala Leu Glu Thr Gly Met Gln Asn Thr Gln Leu Cys Ser
260 265 270
Thr Ile Val Gln Leu Ser Phe Ser Pro Glu Asp Leu Thr Tyr Val Phe
275 280 285
Thr Phe Pro Leu Ile Tyr Ser Ile Phe Gln Ile Ala Phe Ala Ala Ile
290 295 300
Phe Leu Gly Ile Tyr Val Ala Tyr Arg Lys Cys His Gly Lys Asn Asp
305 310 315 320
Ala Glu Phe Pro Asp Ile Lys Asp Thr Lys Thr Glu Pro Glu Ser Ser
325 330 335
Phe His Gln Met Asn Gly Gly Phe Gln Pro Glu
340 345

<210> 42

<211> 348

<212> PRT

<213> Rattus norvegicus

<400> 42

Met Asp Asn Ser Ser Val Cys Ser Pro Asn Ala Thr Phe Cys Glu Gly
1 5 10 15
Asp Ser Cys Leu Val Thr Glu Ser Asn Phe Asn Ala Ile Leu Ser Thr
20 25 30
Val Met Ser Thr Val Leu Thr Ile Leu Leu Ala Met Val Met Phe Ser
35 40 45
Met Gly Cys Asn Val Glu Ile Asn Lys Phe Leu Gly His Ile Lys Arg
50 55 60
Pro Trp Gly Ile Phe Val Gly Phe Leu Cys Gln Phe Gly Ile Met Pro
65 70 75 80
Leu Thr Gly Phe Ile Leu Ser Val Ala Ser Gly Ile Leu Pro Val Gln
85 90 95
Ala Val Val Val Leu Ile Met Gly Cys Cys Pro Gly Gly Thr Gly Ser
100 105 110
Asn Ile Leu Ala Tyr Trp Ile Asp Gly Asp Met Asp Leu Ser Val Ser
115 120 125
Met Thr Thr Cys Ser Thr Leu Leu Ala Leu Gly Met Met Pro Leu Cys
130 135 140
Leu Phe Ile Tyr Thr Lys Met Trp Val Asp Ser Gly Thr Ile Val Ile
145 150 155 160

Cura 468 SEQ list 0705

Pro Tyr Asp Ser Ile Gly Ile Ser Leu Val Ala Leu Val Ile Pro Val
165 170 175
Ser Ile Gly Met Phe Val Asn His Lys Trp Pro Gln Lys Ala Lys Ile
180 185 190
Ile Leu Lys Ile Gly Ser Ile Ala Gly Ala Ile Leu Ile Val Leu Ile
195 200 205
Ala Val Val Gly Gly Ile Leu Tyr Gln Ser Ala Trp Ile Ile Glu Pro
210 215 220
Lys Leu Trp Ile Ile Gly Thr Ile Phe Pro Ile Ala Gly Tyr Ser Leu
225 230 235 240
Gly Phe Phe Leu Ala Arg Leu Ala Gly Gln Pro Trp Tyr Arg Cys Arg
245 250 255
Thr Val Ala Leu Glu Thr Gly Met Gln Asn Thr Gln Leu Cys Ser Thr
260 265 270
Ile Val Gln Leu Ser Phe Ser Pro Glu Asp Leu Asn Leu Val Phe Thr
275 280 285
Phe Pro Leu Ile Tyr Thr Val Phe Gln Leu Val Phe Ala Ala Ile Ile
290 295 300
Leu Gly Met Tyr Val Thr Tyr Lys Lys Cys His Gly Lys Asn Asp Ala
305 310 315 320
Glu Phe Leu Glu Lys Thr Asp Asn Asp Met Asp Pro Met Pro Ser Phe
325 330 335
Gln Glu Thr Asn Lys Gly Phe Gln Pro Asp Glu Lys
340 345

<210> 43
<211> 348
<212> PRT
<213> Mus musculus

<400> 43
Met Asp Asn Ser Ser Val Cys Pro Pro Asn Ala Thr Val Cys Glu Gly
1 5 10 15
Asp Ser Cys Val Val Pro Glu Ser Asn Phe Asn Ala Ile Leu Asn Thr
20 25 30
Val Met Ser Thr Val Leu Thr Ile Leu Leu Ala Met Val Met Phe Ser
35 40 45
Met Gly Cys Asn Val Glu Val His Lys Phe Leu Gly His Ile Lys Arg
50 55 60
Pro Trp Gly Ile Phe Val Gly Phe Leu Cys Gln Phe Gly Ile Met Pro
65 70 75 80
Leu Thr Gly Phe Ile Leu Ser Val Ala Ser Gly Ile Leu Pro Val Gln
85 90 95
Ala Val Val Val Leu Ile Met Gly Cys Cys Pro Gly Gly Thr Gly Ser
100 105 110

Cura 468 SEQ list 0705

Asn Ile Leu Ala Tyr Trp Ile Asp Gly Asp Met Asp Leu Ser Val Ser
115 120 125
Met Thr Thr Cys Ser Thr Leu Leu Ala Leu Gly Met Met Pro Leu Cys
130 135 140
Leu Phe Val Tyr Thr Lys Met Trp Val Asp Ser Gly Thr Ile Val Ile
145 150 155 160
Pro Tyr Asp Ser Ile Gly Ile Ser Leu Val Ala Leu Val Ile Pro Val
165 170 175
Ser Phe Gly Met Phe Val Asn His Lys Trp Pro Gln Lys Ala Lys Ile
180 185 190
Ile Leu Lys Ile Gly Ser Ile Thr Gly Val Ile Leu Ile Val Leu Ile
195 200 205
Ala Val Ile Gly Gly Ile Leu Tyr Gln Ser Ala Trp Ile Ile Glu Pro
210 215 220
Lys Leu Trp Ile Ile Gly Thr Ile Phe Pro Ile Ala Gly Tyr Ser Leu
225 230 235 240
Gly Phe Phe Leu Ala Arg Leu Ala Gly Gln Pro Trp Tyr Arg Cys Arg
245 250 255
Thr Val Ala Leu Glu Thr Gly Met Gln Asn Thr Gln Leu Cys Ser Thr
260 265 270
Ile Val Gln Leu Ser Phe Ser Pro Glu Asp Leu Asn Leu Val Phe Thr
275 280 285
Phe Pro Leu Ile Tyr Thr Val Phe Gln Leu Val Phe Ala Ala Val Ile
290 295 300
Leu Gly Ile Tyr Val Thr Tyr Arg Lys Cys Tyr Gly Lys Asn Asp Ala
305 310 315 320
Glu Phe Leu Glu Lys Thr Asp Asn Glu Met Asp Ser Arg Pro Ser Phe
325 330 335
Asp Glu Thr Asn Lys Gly Phe Gln Pro Asp Glu Lys
340 345

<210> 44
<211> 348
<212> PRT
<213> Mus musculus

<400> 44
Met Asp Asn Ser Ser Val Cys Pro Pro Asn Ala Thr Val Cys Glu Gly
1 5 10 15
Asp Ser Cys Val Val Pro Glu Ser Asn Phe Asn Ala Ile Leu Asn Thr
20 25 30
Val Met Ser Thr Val Leu Thr Ile Leu Leu Ala Met Val Met Phe Ser
35 40 45
Met Gly Cys Asn Val Glu Val His Lys Phe Leu Gly His Ile Lys Arg

Cura 468 SEQ list 0705
60

50 55
Pro Trp Gly Ile Phe Val Gly Phe Leu Cys Gln Phe Gly Ile Met Pro
65 70 75 80
Leu Thr Gly Phe Ile Leu Ser Val Ala Ser Gly Ile Leu Pro Val Gln
85 90 95
Ala Val Val Val Leu Ile Met Gly Cys Cys Pro Gly Gly Thr Gly Ser
100 105 110
Asn Ile Leu Ala Tyr Trp Ile Asp Gly Asp Met Asp Leu Ser Val Ser
115 120 125
Met Thr Thr Cys Ser Thr Leu Leu Ala Leu Gly Met Met Pro Leu Cys
130 135 140
Leu Phe Val Tyr Thr Lys Met Trp Val Asp Ser Gly Thr Ile Val Ile
145 150 155 160
Pro Tyr Asp Ser Ile Gly Ile Ser Leu Val Ala Leu Val Ile Pro Val
165 170 175
Ser Phe Gly Met Phe Val Asn His Lys Trp Pro Gln Lys Ala Lys Ile
180 185 190
Ile Leu Lys Ile Gly Ser Ile Thr Gly Val Ile Leu Ile Val Leu Ile
195 200 205
Ala Val Ile Gly Gly Ile Leu Tyr Gln Ser Ala Trp Ile Ile Glu Pro
210 215 220
Lys Leu Trp Ile Ile Gly Thr Ile Phe Pro Ile Ala Gly Tyr Ser Leu
225 230 235 240
Gly Phe Phe Leu Ala Arg Leu Ala Gly Gln Pro Trp Tyr Arg Cys Arg
245 250 255
Thr Val Ala Leu Glu Thr Gly Met Gln Asn Thr Gln Leu Cys Ser Thr
260 265 270
Ile Val Gln Leu Ser Phe Ser Pro Glu Asp Leu Asn Leu Val Phe Thr
275 280 285
Phe Pro Leu Ile Tyr Thr Val Phe Gln Leu Val Phe Ala Ala Val Ile
290 295 300
Leu Gly Ile Tyr Val Thr Tyr Arg Lys Cys Tyr Gly Lys Asn Asp Ala
305 310 315 320
Glu Phe Leu Glu Lys Thr Asp Asn Glu Met Asp Ser Arg Pro Ser Phe
325 330 335
Asp Glu Thr Asn Lys Gly Phe Gln Pro Asp Glu Lys
340 345

<210> 45
<211> 348
<212> PRT
<213> Homo sapiens

<400> 45

Cura 468 SEQ list 0705

Met Asp Asn Ser Ser Ile Cys Asn Pro Asn Ala Thr Ile Cys Glu Gly
 1 5 10 15
 Asp Ser Cys Ile Ala Pro Glu Ser Asn Phe Asn Ala Ile Leu Ser Val
 20 25 30
 Val Met Ser Thr Val Leu Thr Ile Leu Leu Ala Leu Val Met Phe Ser
 35 40 45
 Met Gly Cys Asn Val Glu Leu His Lys Phe Leu Gly His Leu Arg Arg
 50 55 60
 Pro Trp Gly Ile Val Val Gly Phe Leu Cys Gln Phe Gly Ile Met Pro
 65 70 75 80
 Leu Thr Gly Phe Val Leu Ser Val Ala Phe Gly Ile Leu Pro Val Gln
 85 90 95
 Ala Val Val Val Leu Ile Gln Gly Cys Cys Pro Gly Gly Thr Ala Ser
 100 105 110
 Asn Ile Leu Ala Tyr Trp Val Asp Gly Asp Met Asp Leu Ser Val Ser
 115 120 125
 Met Thr Thr Cys Ser Thr Leu Leu Ala Leu Gly Met Met Pro Leu Cys
 130 135 140
 Leu Phe Ile Tyr Thr Lys Met Trp Val Asp Ser Gly Thr Ile Val Ile
 145 150 155 160
 Pro Tyr Asp Ser Ile Gly Thr Ser Leu Val Ala Leu Val Ile Pro Val
 165 170 175
 Ser Ile Gly Met Tyr Val Asn His Lys Trp Pro Gln Lys Ala Lys Ile
 180 185 190
 Ile Leu Lys Ile Gly Ser Ile Ala Gly Ala Ile Leu Ile Val Leu Ile
 195 200 205
 Ala Val Val Gly Gly Ile Leu Tyr Gln Ser Ala Trp Thr Ile Glu Pro
 210 215 220
 Lys Leu Trp Ile Ile Gly Thr Ile Tyr Pro Ile Ala Gly Tyr Gly Leu
 225 230 235 240
 Gly Phe Phe Leu Ala Arg Ile Ala Gly Gln Pro Trp Tyr Arg Cys Arg
 245 250 255
 Thr Val Ala Leu Glu Thr Gly Leu Gln Asn Thr Gln Leu Cys Ser Thr
 260 265 270
 Ile Val Gln Leu Ser Phe Ser Pro Glu Asp Leu Asn Leu Val Phe Thr
 275 280 285
 Phe Pro Leu Ile Tyr Ser Ile Phe Gln Ile Ala Phe Ala Ala Ile Leu
 290 295 300
 Leu Gly Ala Tyr Val Ala Tyr Lys Lys Cys His Gly Lys Asn Asn Thr
 305 310 315 320
 Glu Leu Gln Glu Lys Thr Asp Asn Glu Met Glu Pro Arg Ser Ser Phe
 325 330 335

Gln Glu Thr Asn Lys Gly Phe Gln Pro Asp Glu Lys
 340 345 Cura 468 SEQ list 0705

<210> 46
 <211> 272
 <212> PRT
 <213> Homo sapiens

<400> 46
 Met Ala Ala Lys Val Phe Glu Ser Ile Gly Lys Phe Gly Leu Ala Leu
 1 5 10 15
 Ala Val Ala Gly Gly Val Val Asn Ser Ala Leu Tyr Asn Val Asp Ala
 20 25 30
 Gly His Arg Ala Val Ile Phe Asp Arg Phe Arg Gly Val Gln Asp Ile
 35 40 45
 Val Val Gly Glu Gly Thr His Phe Leu Ile Pro Trp Val Gln Lys Pro
 50 55 60
 Ile Ile Phe Asp Cys Arg Ser Arg Pro Arg Asn Val Pro Val Ile Thr
 65 70 75 80
 Gly Ser Lys Asp Leu Gln Asn Val Asn Ile Thr Leu Arg Ile Leu Phe
 85 90 95
 Arg Pro Val Ala Ser Gln Leu Pro Arg Ile Phe Thr Ser Ile Gly Glu
 100 105 110
 Asp Tyr Asp Glu Arg Val Leu Pro Ser Ile Thr Thr Glu Ile Leu Lys
 115 120 125
 Ser Val Val Ala Arg Phe Asp Ala Gly Glu Leu Ile Thr Gln Arg Glu
 130 135 140
 Leu Val Ser Arg Gln Val Ser Asp Asp Leu Thr Glu Arg Ala Ala Thr
 145 150 155 160
 Phe Gly Leu Ile Leu Asp Asp Val Ser Leu Thr His Leu Thr Phe Gly
 165 170 175
 Lys Glu Phe Thr Glu Ala Val Glu Ala Lys Gln Val Ala Gln Gln Glu
 180 185 190
 Ala Glu Arg Ala Arg Phe Val Val Glu Lys Ala Glu Gln Gln Lys Lys
 195 200 205
 Ala Ala Ile Ile Ser Ala Glu Gly Asp Ser Lys Ala Ala Glu Leu Ile
 210 215 220
 Ala Asn Ser Leu Ala Thr Ala Gly Asp Gly Leu Ile Glu Leu Arg Lys
 225 230 235 240
 Leu Glu Ala Ala Glu Asp Ile Ala Tyr Gln Leu Ser Arg Ser Arg Asn
 245 250 255
 Ile Thr Tyr Leu Pro Ala Gly Gln Ser Val Leu Leu Gln Leu Pro Gln
 260 265 270

Cura 468 SEQ list 0705

<210> 47
 <211> 272
 <212> PRT
 <213> Rattus norvegicus

<400> 47
 Met Ala Ala Lys Val Phe Glu Ser Ile Gly Lys Phe Gly Leu Ala Leu
 1 5 10 15
 Ala Val Ala Gly Gly Val Val Asn Ser Ala Leu Tyr Asn Val Asp Ala
 20 25 30
 Gly His Arg Ala Val Ile Phe Asp Arg Phe Arg Gly Val Gln Asp Ile
 35 40 45
 Val Val Gly Glu Gly Thr His Phe Leu Ile Pro Trp Val Gln Lys Pro
 50 55 60
 Ile Ile Phe Asp Cys Arg Ser Arg Pro Arg Asn Val Pro Val Ile Thr
 65 70 75 80
 Gly Ser Lys Asp Leu Gln Asn Val Asn Ile Thr Leu Arg Ile Leu Phe
 85 90 95
 Arg Pro Val Ala Ser Gln Leu Pro Arg Ile Tyr Thr Ser Ile Gly Glu
 100 105 110
 Asp Tyr Asp Glu Arg Val Leu Pro Ser Ile Thr Thr Glu Ile Leu Lys
 115 120 125
 Ser Val Val Ala Arg Phe Asp Ala Gly Glu Leu Ile Thr Gln Arg Glu
 130 135 140
 Leu Val Ser Arg Gln Val Ser Asp Asp Leu Thr Glu Arg Ala Ala Thr
 145 150 155 160
 Phe Gly Leu Ile Leu Asp Asp Val Ser Leu Thr His Leu Thr Phe Gly
 165 170 175
 Lys Glu Phe Thr Glu Ala Val Glu Ala Lys Gln Val Ala Gln Gln Glu
 180 185 190
 Ala Glu Arg Ala Arg Phe Val Val Glu Lys Ala Glu Gln Gln Lys Lys
 195 200 205
 Ala Ala Ile Ile Ser Ala Glu Gly Asp Ser Lys Ala Ala Glu Leu Ile
 210 215 220
 Ala Asn Ser Leu Ala Thr Ala Gly Asp Gly Leu Ile Glu Leu Arg Lys
 225 230 235 240
 Leu Glu Ala Ala Glu Asp Ile Ala Tyr Gln Leu Ser Arg Ser Arg Asn
 245 250 255
 Ile Thr Tyr Leu Pro Ala Gly Gln Ser Val Leu Leu Gln Leu Pro Gln
 260 265 270

Cura 468 SEQ list 0705

<210> 48

<211> 1798

<212> PRT

<213> *Drosophila melanogaster*

<400> 48

Met Glu Met Arg Glu Val Leu Ser Arg Glu Gly Arg Glu Ala Lys Asn
 1 5 10 15
 Leu Leu Val Tyr Gln Phe Cys Asp Glu Thr Thr Ser Ser Gly Ala Thr
 20 25 30
 Ser Gly Phe Gly Ser Thr Gly Gly Asp Val Gly Gly Gly Ser Gly Gly
 35 40 45
 Asp Gly Pro Ala Val Gly Ser Gly Gly Val Leu Leu Asn Gly Asp Cys
 50 55 60
 Tyr Arg Lys Pro Pro Met Val Pro Pro Lys Ser Pro Asn Gly Thr Pro
 65 70 75 80
 Lys Asn Cys Gln Ser Pro Thr Ser Pro Arg Leu Lys Ser Ser Ala Ser
 85 90 95
 Val Gly Cys Gly Gly Gly Ser Ser Gly Gly Pro Arg Val Arg Ser Ala
 100 105 110
 Ser Thr Gly Arg Asp Lys Lys Ser Glu Leu Gln Ala Arg Tyr Trp Ala
 115 120 125
 Leu Leu Phe Gly Asn Leu Gln Arg Ala Ile Asn Glu Ile Tyr Gln Thr
 130 135 140
 Val Glu Cys Tyr Glu Asn Ile Ser Ser Cys Gln Glu Thr Ile Leu Val
 145 150 155 160
 Leu Glu Asn Tyr Val Arg Asp Phe Lys Ala Leu Cys Glu Trp Phe Lys
 165 170 175
 Val Ser Trp Asp Tyr Glu Ser Arg Pro Leu Gln Gln Arg Pro Gln Ser
 180 185 190
 Leu Ala Trp Glu Val Arg Lys Ser Asn Pro Thr Pro Arg Val Arg Thr
 195 200 205
 Arg Ser Leu Cys Ser Pro Asn Asn Ser Gly Lys Ser Ser Pro Ala Leu
 210 215 220
 Phe Pro Gly Thr Gln Ser Gly Glu Thr Ser Pro Phe Cys Asp Asn Gly
 225 230 235 240
 Gln Ile Ser Pro Arg Lys Leu Leu Arg Ala Tyr Asp Gln Val Pro Lys
 245 250 255
 Gly Ala Met Arg Leu Asn Val Arg Glu Leu Phe Ala Ala Ser Lys Arg
 260 265 270
 Ala Thr Gln Gly Ser Ser Gln Ser Asp Asn Met Glu Gly Pro Leu Asp
 275 280 285
 Leu Ser Gly Asp Lys Ser Asn Phe Val Leu Arg Ser Thr Gln Tyr Ala
 290 295 300

Cura 468 SEQ list 0705

Gln Thr Asp Leu Glu Asp Pro His Leu Thr Leu Ala Asp Val Arg Glu
305 310 315 320

Lys Met Arg Met Glu Ala Glu Glu Arg Glu Ala Gln Asn Arg Ile Glu
325 330 335

Asn Glu Ala Leu Glu Glu Val Thr Ile Pro Ile Asp Asn Glu Asp Ala
340 345 350

Thr Glu Ser Leu Asn Lys Gln Glu Pro Ser Ser Leu Glu Leu Pro Ile
355 360 365

His Asn Val Ala Asp Leu Ser Lys Glu Pro Glu Leu Met Glu Ala Ala
370 375 380

Ser Glu Ala Thr Ala Leu Glu Met Thr Val Ala Ser Leu Glu Ser Met
385 390 395 400

Glu Asn Ala Leu Leu Asn Gln Gln Ala Asn Lys Glu Pro Thr Pro Pro
405 410 415

Ser Thr Val Ile Lys Pro Leu Ala Glu Ile Leu Lys Lys Pro Gln Pro
420 425 430

Leu Asn Pro Leu Ser Gly Asn Asn Val Gln Asn Ser Pro Leu Lys Tyr
435 440 445

Ser Ser Val Leu Asn Arg Pro Ser Lys Lys Met Ile Pro Pro Pro Gly
450 455 460

Gly Val Ala Ala Gln Lys Thr Ile Ser Thr Lys Pro Gly Leu Val Lys
465 470 475 480

Pro Asn Leu Thr Thr Thr Val Asn Gly Leu Arg Ser Thr Lys Thr Ala
485 490 495

Thr Ala Pro Pro Ala Ile Lys Thr Thr Gly Arg Ser Gly Leu Gln Arg
500 505 510

His Pro Arg Pro Ser Ser Lys Thr Glu Cys Tyr Gly Pro Pro Asn Asn
515 520 525

Val Ala Ser Arg Leu Ser Ala Arg Ser Arg Thr Ile Asn Thr Leu Lys
530 535 540

Ala Glu Asn Gln His Ser Glu Pro Lys Gln Ile Gln Pro Pro Thr Asp
545 550 555 560

Ala Asp Asp Gly Trp Leu Thr Val Lys Asn Arg Arg Arg Thr Ser Met
565 570 575

His Trp Ala Asn Arg Phe Asn Gln Pro Thr Gly Tyr Ala Ser Leu Pro
580 585 590

Thr Leu Ala Leu Leu Asn Glu Gln Gln Lys Glu Gln Glu His Lys Glu
595 600 605

Lys Gln Lys Gly Glu Asp Asp Gly Lys Val Ile Val Lys Thr Ile Ser
610 615 620

Ala Lys Thr Lys Ala Pro Ile Glu Val Ala Lys Ala Lys Ala Lys Thr
625 630 635 640

Cura 468 SEQ list 0705

Ser Ile Val Ile Thr Arg Pro Glu Ile Lys Asn Ala Lys Ala Lys Val
 645 650 655
 Asn Ser Phe Pro Val Gln Lys Ser Asn Thr Asn Gln Val Lys Lys Pro
 660 665 670
 Glu Lys Gln Glu Lys Ser Asp Thr Thr Ala Pro Ala Ala Ile Ala Ser
 675 680 685
 Ser Arg Leu Lys Met Thr Ser Leu His Lys Glu Tyr Met Arg Ser Glu
 690 695 700
 Lys Asn Ala Leu Arg Lys Leu Gln Gln Lys Glu Gln Gly Asn Gln Gln
 705 710 715 720
 His Asn Ser Ser Ser Ser Ser Ala Glu Thr Val Val Glu Ser Cys Asn
 725 730 735
 Glu Asp His Ser Lys Ile Asp Ile Lys Ile Gln Thr Asn Cys Glu Phe
 740 745 750
 Ser Lys Thr Ile Gly Glu Leu Tyr Glu Ser Ile Ala His Cys Lys Leu
 755 760 765
 Pro Ser Gly Ser Leu Lys Thr Asn Ala Ser Thr Leu Ser Ala Cys Asp
 770 775 780
 Glu Asn Glu Glu Gln Asn Thr Asp Asp Asn Glu Glu Glu Arg Asn Glu
 785 790 795 800
 Arg Ile Leu Gly Glu Val Gln Glu Ser Leu Glu Arg Gln Ile Arg Glu
 805 810 815
 Leu Glu Gln Thr Glu Ile Asp Val Asp Thr Glu Thr Asp Glu Thr Asp
 820 825 830
 Cys Glu Val Gln Leu Glu Glu Gln Asp Asp Gly Val Asp Gly Leu Glu
 835 840 845
 Met Gly Ser Gly Asp Asp Ser Ala Val Phe Val Thr Met Ser Asp Asp
 850 855 860
 Glu Asn Ala Ser Leu Glu Leu Arg Tyr Gln Ala Leu Leu Ser Asp Met
 865 870 875 880
 Ser Trp Asn Glu Arg Ala Glu Ala Leu Ala Thr Leu Gln Ala Tyr Val
 885 890 895
 Ala Arg His Pro Gly Arg Ala Gln Glu Leu His Gln Lys Leu Ser Ser
 900 905 910
 Pro Ser Arg Arg Arg Ser Leu Gln Glu Thr Leu Lys Lys Tyr Gln Ala
 915 920 925
 Lys Gln Ala Arg Ala Gln Gln Lys Arg Asn Leu Leu Gln Gln Glu Lys
 930 935 940
 Ala Ala Lys Leu Gln Gln Leu Phe Ser Arg Val Glu Asp Val Lys Ala
 945 950 955 960
 Ala Lys Asn Gln Ile Ile Glu Asp Lys Arg Gln Lys Met Gln Gly Arg
 965 970 975

Cura 468 SEQ list 0705

Leu Gln Arg Ala Ala Glu Asn Arg Glu Gln Tyr Leu Lys Gln Ile Ile
 980 985 990
 Glu Lys Ala His Asp Glu Glu Lys Lys Leu Lys Glu Ile Asn Phe Ile
 995 1000 1005
 Lys Asn Ile Glu Ala Gln Asn Lys Arg Leu Asp Leu Leu Glu Ser Ser
 1010 1015 1020
 Lys Glu Thr Glu Gly Arg Leu Gln Asp Leu Glu Gln Glu Arg Gln Lys
 1025 1030 1035 1040
 Arg Val Glu Glu Lys Leu Ala Lys Glu Ala Ala Val Glu Arg Arg Arg
 1045 1050 1055
 Gln Ala Leu Glu Lys Glu Arg Leu Leu Lys Leu Glu Lys Met Asn Glu
 1060 1065 1070
 Thr Arg Leu Glu Lys Glu Gln Arg Ile Gly Lys Met Gln Glu Gln Lys
 1075 1080 1085
 Glu Lys Gln Arg Gln Ala Leu Ala Arg Glu Lys Ala Arg Asp Arg Glu
 1090 1095 1100
 Glu Arg Leu Leu Ala Leu Gln Val Gln Gln Gln Gln Thr Thr Glu Glu
 1105 1110 1115 1120
 Leu Gln Arg Lys Ile Leu Gln Lys Gln Met Glu Ser Ala Arg Arg His
 1125 1130 1135
 Glu Glu Asn Ile Glu His Ile Arg Gln Arg Ala Leu Glu Leu Thr Ile
 1140 1145 1150
 Pro Thr Arg Gln Ala Asp Glu Gly Arg Gly Asp Gln Asp Val Ser Glu
 1155 1160 1165
 Asp Ile Leu Asn Gly Asn Ala Thr Ser Thr Thr Asn Glu Asp Cys Asp
 1170 1175 1180
 Leu Ser Ser Ser Leu Ser Glu Val Gly Gly Asn Asn Ala His Thr Arg
 1185 1190 1195 1200
 Ser Tyr Lys Lys Lys Met Lys Lys Leu Lys Gln Arg Met Asn Gln Cys
 1205 1210 1215
 Ala Ala Glu Tyr Leu Glu Ser Leu Glu Ala Leu Pro Ala His Ala Arg
 1220 1225 1230
 Arg Asp Ser Thr Val Pro Lys Leu Leu Asn Leu Val Val Lys Gly Gly
 1235 1240 1245
 Gly Ala Gln Gly Leu Asp Arg Asn Leu Gly Asn Leu Leu Arg Val Ile
 1250 1255 1260
 Pro Lys Ala Gln Thr Leu Asp Phe Leu Ala Phe Leu Cys Met Asp Gly
 1265 1270 1275 1280
 Leu Gly Ile Leu Ala Asn His Val Ile Ser Lys Gly Met Asp Glu Asn
 1285 1290 1295
 Ser Glu Ile Ser Arg Lys Ser Val Tyr Leu Ala Ala Gln Leu Tyr Arg
 1300 1305 1310

Cura 468 SEQ list 0705

Asn Ala Cys Ser Val Cys Pro Gln Ile Ala Arg His Ala Leu Leu Gly
1315 1320 1325

Asn Ser Ile Thr Val Leu Phe Asp Ala Ile Asn Lys Ser Phe Gln Val
1330 1335 1340

Ile Leu Lys Ser Asn Arg Cys Thr Lys Glu Thr Phe Ser Asn Phe Trp
1345 1350 1355 1360

Pro Pro Lys Met Leu His Asn Lys Ser Val Ala Arg Gln Ser Ser Arg
1365 1370 1375

Leu Glu Ala Leu Ser Leu Pro Glu Glu Lys Ser Pro Gln His Pro Val
1380 1385 1390

Glu Leu Ser Thr Glu Leu Met Leu Ala Cys Thr Glu Ala Leu Ser Ser
1395 1400 1405

Ser Tyr Val Lys Lys Asn Thr His Pro Lys Val Pro Glu Arg Leu Pro
1410 1415 1420

Asp Met Ile Asn Asp Cys Arg Phe His Trp Gln Asp Val Asn Lys Glu
1425 1430 1435 1440

Asp Met Leu Ala Asp Glu Phe Arg Lys Tyr Lys Cys Tyr Glu Lys Asn
1445 1450 1455

Pro Val Ile Ala Leu Pro His Pro Ser Leu Ser Ala Ser Leu Cys Arg
1460 1465 1470

Ser Leu Ser Ala Thr Pro Leu Lys Ile Asn Leu His Gln Phe Leu Gly
1475 1480 1485

Ser Gly Ile Leu Ile Leu Arg Leu Asn His His Arg His Pro Ala Thr
1490 1495 1500

Gly Ala Ser Phe Ser Asp Ser Cys Cys Thr Cys Cys Pro Lys Leu Thr
1505 1510 1515 1520

Thr Glu Ala Ala Val Ala Ala Val Ala Ala His Gln His Gln His Gln
1525 1530 1535

Asn Gln Gln Gln Gln Pro Asp Tyr Ala Val Ile Thr Gly Leu Ile Glu
1540 1545 1550

Ile Leu Ser Arg Arg Ile Gln Lys Val Arg Glu Ser Ile Glu Ser Asn
1555 1560 1565

Lys Ser Val Met Leu Ser Leu Leu Thr Thr Leu Gly Phe Leu Ser Arg
1570 1575 1580

Phe Ile Asp Val Cys Gln Pro Gly Pro Ala Asp Pro Thr Arg Leu Leu
1585 1590 1595 1600

Ser Ala Ala Lys Ser Thr Glu Leu Phe Gly Thr Val Ser Met Leu Tyr
1605 1610 1615

Gly Cys Val Met Pro Met Gly Glu Cys Ile Pro Pro Arg Thr Thr Ala
1620 1625 1630

Leu Ala Ala Ser Thr Phe His Leu Tyr Val Ser Leu Ala Ser Leu Asp
1635 1640 1645

Cura 468 SEQ list 0705

Val Asn Thr Phe Gln Glu Thr Leu Thr Val Glu Gly Pro Leu Ser Leu
 1650 1655 1660
 Lys Leu Leu Asp Val Met Thr Val Ile Leu Asn Cys Ser Leu Val Asn
 1665 1670 1675 1680
 Asp Gln Trp Thr Thr Asn Ser Glu Ser Cys Pro Met Leu Ile Asp Leu
 1685 1690 1695
 Val Ala Ser Met Ala Phe Phe Cys Val Asn Asn Arg Arg His Gln Asp
 1700 1705 1710
 Leu Leu Ile Ser Glu Gln Tyr Ala Val Ile Phe Lys Arg Met Ala Lys
 1715 1720 1725
 Leu Pro Thr Gln Phe Asn Pro Val Ile Tyr Pro Phe Leu Val Thr Val
 1730 1735 1740
 Ser Phe Asn Asn Pro Pro Ala Arg Glu Phe Leu Ser Lys Asp Phe Asp
 1745 1750 1755 1760
 Leu Thr Phe Leu Asp Glu Tyr Ser Lys Ser Glu Met Ala Gln Arg Asn
 1765 1770 1775
 Val Val Ile Lys Leu Ile Asn Ser Arg Thr Lys Asp Lys Ile Ser Ala
 1780 1785 1790
 Gly Asn Lys Lys Asn Ala
 1795

<210> 49
 <211> 274
 <212> PRT
 <213> Toxocara canis

<400> 49
 Met Ala Gly Ala Gln Lys Leu Leu Gly Arg Leu Gly Gln Ile Gly Val
 1 5 10 15
 Ala Leu Ala Val Thr Gly Gly Val Val Gln Ser Ala Leu Tyr Asn Val
 20 25 30
 Asp Gly Gly Gln Arg Ala Val Ile Phe Asp Arg Phe Thr Gly Val Lys
 35 40 45
 Pro Asp Val Val Gly Glu Gly Thr His Phe Leu Ile Pro Trp Val Gln
 50 55 60
 Arg Pro Ile Ile Phe Asp Ile Arg Ser Thr Pro Arg Ala Ile Ser Thr
 65 70 75 80
 Ile Thr Gly Ser Lys Asp Leu Gln Asn Val Ser Ile Thr Leu Arg Ile
 85 90 95
 Leu His Arg Pro Glu Pro Ser Lys Leu Pro Asn Ile Tyr Leu Asn Ile
 100 105 110
 Gly Gln Asp Tyr Ala Glu Arg Val Leu Pro Ser Ile Thr Asn Glu Val
 115 120 125
 Leu Lys Ala Val Val Ala Gln Phe Asp Ala His Glu Met Ile Thr Gln
 130 135 140

Cura 468 SEQ list 0705

Arg Glu Ser Val Ser His Arg Val Ser Val Glu Leu Ser Glu Arg Ala
 145 150 155 160
 Arg Gln Phe Gly Ile Leu Leu Asp Asp Ile Ala Ile Thr His Leu Ser
 165 170 175
 Phe Gly Arg Glu Phe Thr Glu Ala Val Glu Met Lys Gln Val Ala Gln
 180 185 190
 Gln Glu Ala Glu Lys Ala Arg Tyr Leu Val Glu Thr Ala Glu Gln Met
 195 200 205
 Lys Ile Ala Ala Ile Thr Thr Ala Glu Gly Asp Ala Gln Ala Ala Lys
 210 215 220
 Leu Leu Ala Gln Ala Phe Lys Asp Ala Gly Asp Gly Leu Ile Glu Leu
 225 230 235 240
 Arg Lys Ile Glu Ala Ala Glu Glu Ile Ala Glu Arg Met Ser Lys Thr
 245 250 255
 Arg Asn Val Ile Tyr Leu Pro Gly Asn Gln Asn Thr Leu Phe Asn Leu
 260 265 270

Pro Ala

<210> 50
 <211> 402
 <212> PRT
 <213> Caenorhabditis elegans

<400> 50
 Met Glu Lys Tyr Lys Asn Glu Leu Glu Ile Phe Lys Arg Met Tyr Phe
 1 5 10 15
 Lys Asn Tyr Pro Thr Ser Ser Lys Asp Glu Glu Ala Ala Ala Val Ile
 20 25 30
 Gln Lys Gly Gly Glu Phe Ile Gln Glu Ile Leu Pro Thr Ile Ile Ser
 35 40 45
 Thr Ser Arg Ala Tyr Asp Thr Asn Gln Lys Ala Leu Leu Leu Ala Glu
 50 55 60
 Gly Gly Lys Met Tyr Asn Val Leu Glu Asp Tyr Asn Glu Thr Ala Glu
 65 70 75 80
 Lys Met Leu Ser Lys Ser Val Arg Met Asn Pro Lys Asn Ala Asp Ala
 85 90 95
 Trp His Glu Leu Gly Leu Cys Val Met Lys Arg Arg Asp Leu Glu Phe
 100 105 110
 Ala Gln Ser Cys Phe Lys Ile Ala Leu Gly Ile Ser Lys Thr Ala Pro
 115 120 125
 Ile Leu Thr Ser Leu Ala Val Ala Met Arg Leu Val Ala Leu Glu His
 130 135 140
 Pro Glu Pro Ala Gln Ala Glu Ile Arg Thr Lys Ala Met Glu Leu Ile

Cura 468 SEQ list 0705
155

145 150 160
Ile Glu Ala Arg Arg Leu Asp Ser Ala Tyr Gly Pro Ala Asn Ile Ala
 165 170 175
Phe Ala Thr Gly Leu Phe Tyr Cys Phe Phe Ser Thr Ala Lys Val Glu
 180 185 190
Leu Lys Phe Leu Asp Lys Val Ile Glu Asn Tyr Lys Lys Ala Leu Glu
 195 200 205
Cys Glu Leu Ser Arg Thr Asp Pro Gln Val Tyr Ile Asn Met Ala Thr
 210 215 220
Cys Leu Lys Phe Met Glu Lys Tyr Asp Glu Ala Leu Ala Val Leu Gln
225 230 235 240
Lys Ala Val Glu Tyr Asp Pro Arg Asn Glu Leu Glu Thr Arg Glu Lys
 245 250 255
Leu Ala Ser Phe Val Ser Tyr Leu Ser Lys Phe Thr Asp Ala Ile Gln
 260 265 270
Lys Lys Gly Lys Met Lys Ala Lys Arg Met Gln Glu Met Ile Asn Glu
 275 280 285
Leu Lys Lys Ser Ser Asp Gly Phe Arg Ala Lys Ile Ile Gly Asn Ile
290 295 300
Gly His Asp Glu Thr Ile Pro Val Ala Leu Val Gly Val Asp Ala Ala
305 310 315 320
Gly Glu Val Tyr Gly Ile Thr Ile Tyr Asn Cys Leu Ser Asn Phe Gly
 325 330 335
Phe Val Ile Gly Asp Thr Val Thr Ile Ala Lys Pro Asp Phe Arg Glu
 340 345 350
Ile Lys Asn Leu Thr Ile Pro Ser Asp Pro Glu Ile His Val Asp Ser
 355 360 365
Val Lys Trp Ile Arg Val Ala Thr Pro Thr Gln Met Lys Lys Asn Gly
370 375 380
Val Pro Leu Pro Glu Ser Val Leu Ala Arg Ala Val Ala Ser Thr Gln
385 390 395 400
Thr Lys

<210> 51
<211> 711
<212> PRT
<213> Homo sapiens

<400> 51
Met Gly Trp Leu Pro Leu Leu Leu Leu Leu Thr Gln Cys Leu Gly Val
1 5 10 15
Pro Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Val Leu Arg Gly Thr
20 25 30

Cura 468 SEQ list 0705

Glu Leu Gln His Leu Leu His Ala Val Val Pro Gly Pro Trp Gln Glu
 35 40 45
 Asp Val Ala Asp Ala Glu Glu Cys Ala Gly Arg Cys Gly Pro Leu Met
 50 55 60
 Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln Leu
 65 70 75 80
 Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg Arg Ser Gly
 85 90 95
 Arg Cys Asp Leu Phe Gln Lys Lys Asp Tyr Val Arg Thr Cys Ile Met
 100 105 110
 Asn Asn Gly Val Gly Tyr Arg Gly Thr Met Ala Thr Thr Val Gly Gly
 115 120 125
 Leu Pro Cys Gln Ala Trp Ser His Lys Phe Pro Asn Asp His Lys Tyr
 130 135 140
 Thr Pro Thr Leu Arg Asn Gly Leu Glu Glu Asn Phe Cys Arg Asn Pro
 145 150 155 160
 Asp Gly Asp Pro Gly Gly Pro Trp Cys Tyr Thr Thr Asp Pro Ala Val
 165 170 175
 Arg Phe Gln Ser Cys Gly Ile Lys Ser Cys Arg Glu Ala Ala Cys Val
 180 185 190
 Trp Cys Asn Gly Glu Glu Tyr Arg Gly Ala Val Asp Arg Thr Glu Ser
 195 200 205
 Gly Arg Glu Cys Gln Arg Trp Asp Leu Gln His Pro His Gln His Pro
 210 215 220
 Phe Glu Pro Gly Lys Phe Leu Asp Gln Gly Leu Asp Asp Asn Tyr Cys
 225 230 235 240
 Arg Asn Pro Asp Gly Ser Glu Arg Pro Trp Cys Tyr Thr Thr Asp Pro
 245 250 255
 Gln Ile Glu Arg Glu Phe Cys Asp Leu Pro Arg Cys Gly Ser Glu Ala
 260 265 270
 Gln Pro Arg Gln Glu Ala Thr Thr Val Ser Cys Phe Arg Gly Lys Gly
 275 280 285
 Glu Gly Tyr Arg Gly Thr Ala Asn Thr Thr Thr Ala Gly Val Pro Cys
 290 295 300
 Gln Arg Trp Asp Ala Gln Ile Pro His Gln His Arg Phe Thr Pro Glu
 305 310 315 320
 Lys Tyr Ala Cys Lys Asp Leu Arg Glu Asn Phe Cys Arg Asn Pro Asp
 325 330 335
 Gly Ser Glu Ala Pro Trp Cys Phe Thr Leu Arg Pro Gly Met Arg Ala
 340 345 350
 Ala Phe Cys Tyr Gln Ile Arg Arg Cys Thr Asp Asp Val Arg Pro Gln
 355 360 365

Cura 468 SEQ list 0705

Asp Cys Tyr His Gly Ala Gly Glu Gln Tyr Arg Gly Thr Val Ser Lys
 370 375 380
 Thr Arg Lys Gly Val Gln Cys Gln Arg Trp Ser Ala Glu Thr Pro His
 385 390 395 400
 Lys Pro Gln Phe Thr Phe Thr Ser Glu Pro His Ala Gln Leu Glu Glu
 405 410 415
 Asn Phe Cys Arg Asn Pro Asp Gly Asp Ser His Gly Pro Trp Cys Tyr
 420 425 430
 Thr Met Asp Pro Arg Thr Pro Phe Asp Tyr Cys Ala Leu Arg Arg Cys
 435 440 445
 Ala Asp Asp Gln Pro Pro Ser Ile Leu Asp Pro Pro Asp Gln Val Gln
 450 455 460
 Phe Glu Lys Cys Gly Lys Arg Val Asp Arg Leu Asp Gln Arg Arg Ser
 465 470 475 480
 Lys Leu Arg Val Val Gly Gly His Pro Gly Asn Ser Pro Trp Thr Val
 485 490 495
 Ser Leu Arg Asn Arg Gln Gly Gln His Phe Cys Gly Gly Ser Leu Val
 500 505 510
 Lys Glu Gln Trp Ile Leu Thr Ala Arg Gln Cys Phe Ser Ser Cys His
 515 520 525
 Met Pro Leu Thr Gly Tyr Glu Val Trp Leu Gly Thr Leu Phe Gln Asn
 530 535 540
 Pro Gln His Gly Glu Pro Ser Leu Gln Arg Val Pro Val Ala Lys Met
 545 550 555 560
 Val Cys Gly Pro Ser Gly Ser Gln Leu Val Leu Leu Lys Leu Glu Arg
 565 570 575
 Ser Val Thr Leu Asn Gln Arg Val Ala Leu Ile Cys Leu Pro Pro Glu
 580 585 590
 Trp Tyr Val Val Pro Pro Gly Thr Lys Cys Glu Ile Ala Gly Trp Gly
 595 600 605
 Glu Thr Lys Gly Thr Gly Asn Asp Thr Val Leu Asn Val Ala Leu Leu
 610 615 620
 Asn Val Ile Ser Asn Gln Glu Cys Asn Ile Lys His Arg Gly Arg Val
 625 630 635 640
 Arg Glu Ser Glu Met Cys Thr Glu Gly Leu Leu Ala Pro Val Gly Ala
 645 650 655
 Cys Glu Gly Asp Tyr Gly Gly Pro Leu Ala Cys Phe Thr His Asn Cys
 660 665 670
 Trp Val Leu Glu Gly Ile Ile Ile Pro Asn Arg Val Cys Ala Arg Ser
 675 680 685
 Arg Trp Pro Ala Val Phe Thr Arg Val Ser Val Phe Val Asp Trp Ile
 690 695 700

Cura 468 SEQ list 0705

His Lys Val Met Arg Leu Gly
705 710

<210> 52
<211> 711
<212> PRT
<213> Homo sapiens

<400> 52

Met Gly Trp Leu Pro Leu Leu Leu Leu Leu Thr Gln Cys Leu Gly Val
1 5 10 15
Pro Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Val Leu Arg Gly Thr
20 25 30
Glu Leu Gln His Leu Leu His Ala Val Val Pro Gly Pro Trp Gln Glu
35 40 45
Asp Val Ala Asp Ala Glu Glu Cys Ala Gly Arg Cys Gly Pro Leu Met
50 55 60
Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln Leu
65 70 75 80
Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg Arg Ser Gly
85 90 95
Arg Cys Asp Leu Phe Gln Lys Lys Asp Tyr Val Arg Thr Cys Ile Met
100 105 110
Asn Asn Gly Val Gly Tyr Arg Gly Thr Met Ala Thr Thr Val Gly Gly
115 120 125
Leu Pro Cys Gln Ala Trp Ser His Lys Phe Pro Asn Asp His Lys Tyr
130 135 140
Thr Pro Thr Leu Arg Asn Gly Leu Glu Glu Asn Phe Cys Arg Asn Pro
145 150 155 160
Asp Gly Asp Pro Gly Gly Pro Trp Cys Tyr Thr Thr Asp Pro Ala Val
165 170 175
Arg Phe Gln Ser Cys Gly Ile Lys Ser Cys Arg Glu Ala Ala Cys Val
180 185 190
Trp Cys Asn Gly Glu Glu Tyr Arg Gly Ala Val Asp Arg Thr Glu Ser
195 200 205
Gly Arg Glu Cys Gln Arg Trp Asp Leu Gln His Pro His Gln His Pro
210 215 220
Phe Glu Pro Gly Lys Phe Leu Asp Gln Gly Leu Asp Asp Asn Tyr Cys
225 230 235 240
Arg Asn Pro Asp Gly Ser Glu Arg Pro Trp Cys Tyr Thr Thr Asp Pro
245 250 255
Gln Ile Glu Arg Glu Phe Cys Asp Leu Pro Arg Cys Gly Ser Glu Ala
260 265 270
Gln Pro Arg Gln Glu Ala Thr Thr Val Ser Cys Phe Arg Gly Lys Gly
275 280 285

Cura 468 SEQ list 0705

Glu Gly Tyr Arg Gly Thr Ala Asn Thr Thr Thr Ala Gly Val Pro Cys
 290 295 300
 Gln Arg Trp Asp Ala Gln Ile Pro His Gln His Arg Phe Thr Pro Glu
 305 310 315 320
 Lys Tyr Ala Cys Lys Asp Leu Arg Glu Asn Phe Cys Arg Asn Pro Asp
 325 330 335
 Gly Ser Glu Ala Pro Trp Cys Phe Thr Leu Arg Pro Gly Met Arg Ala
 340 345 350
 Ala Phe Cys Tyr Gln Ile Arg Arg Cys Thr Asp Asp Val Arg Pro Gln
 355 360 365
 Asp Cys Tyr His Gly Ala Gly Glu Gln Tyr Arg Gly Thr Val Ser Lys
 370 375 380
 Thr Arg Lys Gly Val Gln Cys Gln Arg Trp Ser Ala Glu Thr Pro His
 385 390 395 400
 Lys Pro Gln Phe Thr Phe Thr Ser Glu Pro His Ala Gln Leu Glu Glu
 405 410 415
 Asn Phe Cys Arg Asn Pro Asp Gly Asp Ser His Gly Pro Trp Cys Tyr
 420 425 430
 Thr Met Asp Pro Arg Thr Pro Phe Asp Tyr Cys Ala Leu Arg Arg Cys
 435 440 445
 Ala Asp Asp Gln Pro Pro Ser Ile Leu Asp Pro Pro Asp Gln Val Gln
 450 455 460
 Phe Glu Lys Cys Gly Lys Arg Val Asp Arg Leu Asp Gln Arg Arg Ser
 465 470 475 480
 Lys Leu Arg Val Val Gly Gly His Pro Gly Asn Ser Pro Trp Thr Val
 485 490 495
 Ser Leu Arg Asn Arg Gln Gly Gln His Phe Cys Gly Gly Ser Leu Val
 500 505 510
 Lys Glu Gln Trp Ile Leu Thr Ala Arg Gln Cys Phe Ser Ser Cys His
 515 520 525
 Met Pro Leu Thr Gly Tyr Glu Val Trp Leu Gly Thr Leu Phe Gln Asn
 530 535 540
 Pro Gln His Gly Glu Pro Ser Leu Gln Arg Val Pro Val Ala Lys Met
 545 550 555 560
 Val Cys Gly Pro Ser Gly Ser Gln Leu Val Leu Leu Lys Leu Glu Arg
 565 570 575
 Ser Val Thr Leu Asn Gln Arg Val Ala Leu Ile Cys Leu Pro Pro Glu
 580 585 590
 Trp Tyr Val Val Pro Pro Gly Thr Lys Cys Glu Ile Ala Gly Trp Gly
 595 600 605
 Glu Thr Lys Gly Thr Gly Asn Asp Thr Val Leu Asn Val Ala Phe Leu
 610 615 620

Cura 468 SEQ list 0705

Asn Val Ile Ser Asn Gln Glu Cys Asn Ile Lys His Arg Gly Arg Val
 625 630 635 640
 Arg Glu Ser Glu Met Cys Thr Glu Gly Leu Leu Ala Pro Val Gly Ala
 645 650 655
 Cys Glu Gly Asp Tyr Gly Gly Pro Leu Ala Cys Phe Thr His Asn Cys
 660 665 670
 Trp Val Leu Glu Gly Ile Ile Ile Pro Asn Arg Val Cys Ala Arg Ser
 675 680 685
 Arg Trp Pro Ala Val Phe Thr Arg Val Ser Val Phe Val Asp Trp Ile
 690 695 700
 His Lys Val Met Arg Leu Gly
 705 710

<210> 53
 <211> 711
 <212> PRT
 <213> Homo sapiens

<400> 53
 Met Gly Trp Leu Pro Leu Leu Leu Leu Leu Thr Gln Tyr Leu Gly Val
 1 5 10 15
 Pro Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Val Leu Arg Gly Thr
 20 25 30
 Glu Leu Gln His Leu Leu His Ala Val Val Pro Gly Pro Trp Gln Glu
 35 40 45
 Asp Val Ala Asp Ala Glu Glu Cys Ala Gly Arg Cys Gly Pro Leu Met
 50 55 60
 Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln Leu
 65 70 75 80
 Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg Arg Ser Gly
 85 90 95
 Arg Cys Asp Leu Phe Gln Lys Lys Asp Tyr Val Arg Thr Cys Ile Met
 100 105 110
 Asn Asn Gly Val Gly Tyr Arg Gly Thr Met Ala Thr Thr Val Gly Gly
 115 120 125
 Leu Pro Cys Gln Ala Trp Ser His Lys Phe Pro Asn Asp His Lys Tyr
 130 135 140
 Thr Pro Thr Leu Arg Asn Gly Leu Glu Glu Asn Phe Cys Arg Asn Pro
 145 150 155 160
 Asp Gly Asp Pro Gly Gly Pro Trp Cys Tyr Thr Thr Asp Pro Ala Val
 165 170 175
 Arg Phe Gln Ser Cys Gly Ile Lys Ser Cys Arg Glu Ala Ala Cys Val
 180 185 190
 Trp Cys Asn Gly Glu Glu Tyr Arg Gly Ala Val Asp Arg Thr Glu Ser

Cura 468 SEQ list 0705

195 200 205
 Gly Arg Glu Cys Gln Arg Trp Asp Leu Gln His Pro His Gln His Pro
 210 215 220
 Phe Glu Pro Gly Lys Phe Leu Asp Gln Gly Leu Asp Asp Asn Tyr Cys
 225 230 235 240
 Arg Asn Pro Asp Gly Ser Glu Arg Pro Trp Cys Tyr Thr Thr Asp Pro
 245 250 255
 Gln Ile Glu Arg Glu Phe Cys Asp Leu Pro Arg Cys Gly Ser Glu Ala
 260 265 270
 Gln Pro Arg Gln Glu Ala Thr Thr Val Ser Cys Phe Arg Gly Lys Gly
 275 280 285
 Glu Gly Tyr Arg Gly Thr Ala Asn Thr Thr Thr Ala Gly Val Pro Cys
 290 295 300
 Gln Arg Trp Asp Ala Gln Ile Pro His Gln His Arg Phe Thr Pro Glu
 305 310 315 320
 Lys Tyr Ala Cys Lys Asp Leu Arg Glu Asn Phe Cys Arg Asn Pro Asp
 325 330 335
 Gly Ser Glu Ala Pro Trp Cys Phe Thr Leu Arg Pro Gly Met Arg Ala
 340 345 350
 Ala Phe Cys Tyr Gln Ile Arg Arg Cys Thr Asp Asp Val Arg Pro Gln
 355 360 365
 Asp Cys Tyr His Gly Ala Gly Glu Gln Tyr Arg Gly Thr Val Ser Lys
 370 375 380
 Thr Arg Lys Gly Val Gln Cys Gln Arg Trp Ser Ala Glu Thr Pro His
 385 390 395 400
 Lys Pro Gln Phe Thr Phe Thr Ser Glu Pro His Ala Gln Leu Glu Glu
 405 410 415
 Asn Phe Cys Arg Asn Pro Asp Gly Asp Ser His Gly Pro Trp Cys Tyr
 420 425 430
 Thr Met Asp Pro Arg Thr Pro Phe Asp Tyr Cys Ala Leu Arg Arg Cys
 435 440 445
 Ala Asp Asp Gln Pro Pro Ser Ile Leu Asp Pro Pro Asp Gln Val Gln
 450 455 460
 Phe Glu Lys Cys Gly Lys Arg Val Asp Arg Leu Asp Gln Arg Arg Ser
 465 470 475 480
 Lys Leu Arg Val Val Gly Gly His Pro Gly Asn Ser Pro Trp Thr Val
 485 490 495
 Ser Leu Arg Asn Arg Gln Gly Gln His Phe Cys Gly Gly Ser Leu Val
 500 505 510
 Lys Glu Gln Trp Ile Leu Thr Ala Arg Gln Cys Phe Ser Ser Cys His
 515 520 525
 Met Pro Leu Thr Gly Tyr Glu Val Trp Leu Gly Thr Leu Phe Gln Asn

Cura 468 SEQ list 0705

530

535

540

Pro Gln His Gly Glu Pro Ser Leu Gln Arg Val Pro Val Ala Lys Met
 545 550 555 560
 Val Cys Gly Pro Ser Gly Ser Gln Leu Val Leu Leu Lys Leu Glu Arg
 565 570 575
 Ser Val Thr Leu Asn Gln Arg Val Ala Leu Ile Cys Leu Pro Pro Glu
 580 585 590
 Trp Tyr Val Val Pro Pro Gly Thr Lys Cys Glu Ile Ala Gly Trp Gly
 595 600 605
 Glu Thr Lys Gly Thr Gly Asn Asp Thr Val Leu Asn Val Ala Leu Leu
 610 615 620
 Asn Val Ile Ser Asn Gln Glu Cys Asn Ile Lys His Arg Gly Arg Val
 625 630 635 640
 Arg Glu Ser Glu Met Cys Thr Glu Gly Leu Leu Ala Pro Val Gly Ala
 645 650 655
 Cys Glu Gly Asp Tyr Gly Gly Pro Leu Ala Cys Phe Thr His Asn Cys
 660 665 670
 Trp Val Leu Glu Gly Ile Ile Ile Pro Asn Arg Val Cys Ala Arg Ser
 675 680 685
 Arg Trp Pro Ala Val Phe Thr Arg Val Ser Val Phe Val Asp Trp Ile
 690 695 700
 His Lys Val Met Arg Leu Gly
 705 710

<210> 54
 <211> 529
 <212> PRT
 <213> Homo sapiens

<400> 54
 Met Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln
 1 5 10 15
 Leu Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg His Ser
 20 25 30
 Gly Arg Cys Asp Leu Phe Gln Glu Lys Asp Tyr Ile Arg Thr Cys Ile
 35 40 45
 Met Asn Asn Gly Val Gly Tyr Arg Gly Thr Met Ala Thr Thr Val Gly
 50 55 60
 Gly Leu Ser Cys Gln Ala Trp Ser His Lys Phe Pro Asn Asp His Gln
 65 70 75 80
 Tyr Met Pro Thr Leu Arg Asn Gly Leu Glu Glu Asn Phe Cys Arg Asn
 85 90 95
 Pro Asp Gly Asp Pro Gly Gly Pro Trp Cys His Thr Thr Asp Pro Ala
 100 105 110

Cura 468 SEQ list 0705

Val Arg Phe Gln Ser Cys Gly Ile Lys Ser Cys Arg Val Ala Ala Cys
 115 120 125
 Val Trp Cys Asn Gly Glu Glu Tyr Arg Gly Ala Val Asp Arg Thr Glu
 130 135 140
 Ser Gly Arg Glu Cys Gln Arg Trp Asp Leu Gln His Pro His Gln His
 145 150 155 160
 Pro Phe Glu Pro Gly Lys Phe Leu Asp Gln Gly Leu Asp Asp Asn Tyr
 165 170 175
 Cys Arg Asn Pro Asp Gly Ser Glu Arg Pro Trp Cys Tyr Thr Thr Asp
 180 185 190
 Pro Gln Ile Glu Arg Glu Phe Cys Asp Leu Pro Arg Cys Gly Ser Glu
 195 200 205
 Ala Gln Pro Arg Gln Glu Ala Thr Ser Val Ser Cys Phe Arg Gly Lys
 210 215 220
 Gly Glu Gly Tyr Arg Gly Thr Ala Asn Thr Thr Thr Ala Gly Val Pro
 225 230 235 240
 Cys Gln Arg Trp Asp Ala Gln Ile Pro His Gln His Arg Phe Thr Pro
 245 250 255
 Glu Lys Tyr Ala Cys Lys Asp Leu Arg Glu Asn Phe Cys Arg Asn Pro
 260 265 270
 Asp Gly Ser Glu Ala Pro Trp Cys Phe Thr Leu Arg Pro Gly Met Arg
 275 280 285
 Val Gly Phe Cys Tyr Gln Ile Arg Arg Cys Thr Asp Asp Val Arg Pro
 290 295 300
 Gln Asp Cys Tyr His Gly Ala Gly Glu Gln Tyr Arg Gly Thr Val Ser
 305 310 315 320
 Lys Thr Arg Lys Gly Val Gln Cys Gln Arg Gly Ser Ala Glu Thr Pro
 325 330 335
 His Lys Pro Gln Phe Thr Phe Thr Ser Glu Pro His Ala Gln Leu Glu
 340 345 350
 Glu Asn Phe Cys Gln Thr Gln Met Gly Ile Ala Met Gly Pro Gly Ala
 355 360 365
 Thr Arg Trp Thr Gln Gly Pro His Ser Thr Thr Val Pro Cys Asp Ala
 370 375 380
 Ala Leu Met Thr Ser Arg His Gln Ser Trp Thr Pro Gln Thr Arg Cys
 385 390 395 400
 Ser Leu Arg Ser Val Ala Arg Gly Trp Ile Gly Trp Ile Ser Val Val
 405 410 415
 Pro Ser Cys Ala Trp Leu Gly Ala Ile Arg Ala Thr His Pro Gly Gln
 420 425 430
 Ser Ala Cys Gly Ile Gly Gln Gly Gln His Phe Cys Gly Gly Ser Leu
 435 440 445

Cura 468 SEQ list 0705

Val Lys Glu Gln Trp Ile Leu Thr Ala Arg Gln Cys Phe Ser Ser Cys
 450 455 460
 His Met Pro Leu Thr Gly Tyr Glu Val Trp Leu Gly Thr Leu Phe Gln
 465 470 475 480
 Asn Pro Gln His Gly Glu Pro Gly Leu Gln Arg Val Pro Val Ala Lys
 485 490 495
 Met Leu Cys Gly Pro Ser Gly Ser Gln Leu Val Leu Leu Lys Leu Glu
 500 505 510
 Arg Ser Val Thr Leu Asn Gln Arg Val Ala Leu Ile Cys Leu Pro Pro
 515 520 525

Glu

<210> 55
 <211> 716
 <212> PRT
 <213> Mus musculus

<400> 55
 Met Gly Trp Leu Pro Leu Leu Leu Leu Leu Val Gln Cys Ser Arg Ala
 1 5 10 15
 Leu Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Leu Phe Arg Gly Thr
 20 25 30
 Glu Leu Arg Asn Leu Leu His Thr Ala Val Pro Gly Pro Trp Gln Glu
 35 40 45
 Asp Val Ala Asp Ala Glu Glu Cys Ala Arg Arg Cys Gly Pro Leu Leu
 50 55 60
 Asp Cys Arg Ala Phe His Tyr Asn Met Ser Ser His Gly Cys Gln Leu
 65 70 75 80
 Leu Pro Trp Thr Gln His Ser Leu His Thr Gln Leu Tyr His Ser Ser
 85 90 95
 Leu Cys His Leu Phe Gln Lys Lys Asp Tyr Val Arg Thr Cys Ile Met
 100 105 110
 Asp Asn Gly Val Ser Tyr Arg Gly Thr Val Ala Arg Thr Ala Gly Gly
 115 120 125
 Leu Pro Cys Gln Ala Trp Ser Arg Arg Phe Pro Asn Asp His Lys Tyr
 130 135 140
 Thr Pro Thr Pro Lys Asn Gly Leu Glu Glu Asn Phe Cys Arg Asn Pro
 145 150 155 160
 Asp Gly Asp Pro Arg Gly Pro Trp Cys Tyr Thr Thr Asn Arg Ser Val
 165 170 175
 Arg Phe Gln Ser Cys Gly Ile Lys Thr Cys Arg Glu Ala Val Cys Val
 180 185 190
 Leu Cys Asn Gly Glu Asp Tyr Arg Gly Glu Val Asp Val Thr Glu Ser
 195 200 205

Cura 468 SEQ list 0705

Gly Arg Glu Cys Gln Arg Trp Asp Leu Gln His Pro His Ser His Pro
 210 215 220
 Phe Gln Pro Glu Lys Phe Leu Asp Lys Asp Leu Lys Asp Asn Tyr Cys
 225 230 235 240
 Arg Asn Pro Asp Gly Ser Glu Arg Pro Trp Cys Tyr Thr Thr Asp Pro
 245 250 255
 Asn Val Glu Arg Glu Phe Cys Asp Leu Pro Ser Cys Gly Pro Asn Leu
 260 265 270
 Pro Pro Thr Val Lys Gly Ser Lys Ser Gln Arg Arg Asn Lys Gly Lys
 275 280 285
 Ala Leu Asn Cys Phe Arg Gly Lys Gly Glu Asp Tyr Arg Gly Thr Thr
 290 295 300
 Asn Thr Thr Ser Ala Gly Val Pro Cys Gln Arg Trp Asp Ala Gln Ser
 305 310 315 320
 Pro His Gln His Arg Phe Val Pro Glu Lys Tyr Ala Cys Lys Asp Leu
 325 330 335
 Arg Glu Asn Phe Cys Arg Asn Pro Asp Gly Ser Glu Ala Pro Trp Cys
 340 345 350
 Phe Thr Ser Arg Pro Gly Leu Arg Met Ala Phe Cys His Gln Ile Pro
 355 360 365
 Arg Cys Thr Glu Glu Leu Val Pro Glu Gly Cys Tyr His Gly Ser Gly
 370 375 380
 Glu Gln Tyr Arg Gly Ser Val Ser Lys Thr Arg Lys Gly Val Gln Cys
 385 390 395 400
 Gln His Trp Ser Ser Glu Thr Pro His Lys Pro Gln Phe Thr Pro Thr
 405 410 415
 Ser Ala Pro Gln Ala Gly Leu Glu Ala Asn Phe Cys Arg Asn Pro Asp
 420 425 430
 Gly Asp Ser His Gly Pro Trp Cys Tyr Thr Leu Asp Pro Asp Ile Leu
 435 440 445
 Phe Asp Tyr Cys Ala Leu Gln Arg Cys Asp Asp Asp Gln Pro Pro Ser
 450 455 460
 Ile Leu Asp Pro Pro Asp Gln Val Val Phe Glu Lys Cys Gly Lys Arg
 465 470 475 480
 Val Asp Lys Ser Asn Lys Leu Arg Val Val Gly Gly His Pro Gly Asn
 485 490 495
 Ser Pro Trp Thr Val Ser Leu Arg Asn Arg Gln Gly Gln His Phe Cys
 500 505 510
 Gly Gly Ser Leu Val Lys Glu Gln Trp Val Leu Thr Ala Arg Gln Cys
 515 520 525
 Ile Trp Ser Cys His Glu Pro Leu Thr Gly Tyr Glu Val Trp Leu Gly
 530 535 540

Cura 468 SEQ list 0705

Thr Ile Asn Gln Asn Pro Gln Pro Gly Glu Ala Asn Leu Gln Arg Val
545 550 555 560
Pro Val Ala Lys Ala Val Cys Gly Pro Ala Gly Ser Gln Leu Val Leu
565 570 575
Leu Lys Leu Glu Arg Pro Val Ile Leu Asn His His Val Ala Leu Ile
580 585 590
Cys Leu Pro Pro Glu Gln Tyr Val Val Pro Pro Gly Thr Lys Cys Glu
595 600 605
Ile Ala Gly Trp Gly Glu Ser Ile Gly Thr Ser Asn Asn Thr Val Leu
610 615 620
His Val Ala Ser Met Asn Val Ile Ser Asn Gln Glu Cys Asn Thr Lys
625 630 635 640
Tyr Arg Gly His Ile Gln Glu Ser Glu Ile Cys Thr Gln Gly Leu Val
645 650 655
Val Pro Val Gly Ala Cys Glu Gly Asp Tyr Gly Gly Pro Leu Ala Cys
660 665 670
Tyr Thr His Asp Cys Trp Val Leu Gln Gly Leu Ile Ile Pro Asn Arg
675 680 685
Val Cys Ala Arg Pro Arg Trp Pro Ala Ile Phe Thr Arg Val Ser Val
690 695 700
Phe Val Asp Trp Ile Asn Lys Val Met Gln Leu Glu
705 710 715

<210> 56
<211> 135
<212> PRT
<213> Homo sapiens

<400> 56
Met Ala Thr Val Gln Gln Leu Glu Gly Arg Trp Arg Leu Val Asp Ser
1 5 10 15
Lys Gly Phe Asp Glu Tyr Met Lys Glu Leu Gly Val Gly Ile Ala Leu
20 25 30
Arg Lys Met Gly Ala Met Ala Lys Pro Asp Cys Ile Val Thr Cys Asp
35 40 45
Gly Lys Asn Leu Thr Ile Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln
50 55 60
Phe Ser Cys Pro Leu Gly Glu Lys Phe Glu Glu Thr Thr Ala Asp Gly
65 70 75 80
Arg Lys Thr Gln Thr Val Cys Asn Phe Thr Asp Gly Ala Leu Val Gln
85 90 95
His Gln Glu Trp Asp Gly Lys Glu Ser Thr Ile Thr Arg Lys Leu Lys
100 105 110
Asp Gly Lys Leu Val Val Glu Cys Val Met Asn His Val Ala Cys Thr

115

120

125

Arg Ile Tyr Glu Lys Val Glu
130 135

<210> 57

<211> 135

<212> PRT

<213> Homo sapiens

<400> 57

Met Ala Thr Val Gln Gln Leu Glu Gly Arg Trp Arg Leu Val Asp Ser
1 5 10 15

Lys Gly Phe Asp Glu Tyr Met Lys Glu Leu Gly Val Gly Ile Ala Leu
20 25 30

Arg Lys Met Gly Ala Met Ala Lys Pro Asp Cys Ile Ile Thr Cys Asp
35 40 45

Gly Lys Asn Leu Thr Ile Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln
50 55 60

Phe Ser Cys Thr Leu Gly Glu Lys Phe Glu Glu Thr Thr Ala Asp Gly
65 70 75 80

Arg Lys Thr Gln Thr Val Cys Asn Phe Thr Asp Gly Ala Leu Val Gln
85 90 95

His Gln Glu Trp Asp Gly Lys Glu Ser Thr Ile Thr Arg Lys Leu Lys
100 105 110

Asp Gly Lys Leu Val Val Glu Cys Val Met Asn Asn Val Thr Cys Thr
115 120 125

Arg Ile Tyr Glu Lys Val Glu
130 135

<210> 58

<211> 135

<212> PRT

<213> Homo sapiens

<400> 58

Met Ala Thr Val Gln Gln Leu Glu Gly Arg Trp Arg Leu Val Asp Ser
1 5 10 15

Arg Gly Phe Asp Glu Tyr Val Lys Glu Leu Gly Val Gly Ile Ala Leu
20 25 30

Arg Lys Met Asp Thr Ile Ala Lys Pro Asp Cys Ile Ile Thr Cys Asp
35 40 45

Gly Lys Asn Leu Thr Ile Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln
50 55 60

Phe Ser Cys Thr Leu Gly Glu Asn Phe Glu Glu Thr Thr Ala Asp Gly
65 70 75 80

Arg Lys Thr Gln Thr Val Cys Asn Phe Thr Asp Gly Ala Leu Val Gln
85 90 95

Cura 468 SEQ list 0705

His Gln Glu Trp Asp Gly Lys Glu Asn Thr Ile Arg Arg Lys Leu Lys
 100 105 110
 Asp Gly Lys Leu Val Val Asp Cys Val Met Asn Ser Val Thr Cys Thr
 115 120 125
 Arg Ile Tyr Glu Lys Val Glu
 130 135

<210> 59
 <211> 135
 <212> PRT
 <213> Homo sapiens

<400> 59
 Met Ala Thr Val Gln Gln Leu Glu Gly Arg Trp Arg Leu Leu Asp Ser
 1 5 10 15
 Lys Gly Phe Asp Glu Tyr Met Lys Glu Leu Gly Val Gly Ile Ala Leu
 20 25 30
 Gln Lys Met Gly Ala Met Ala Lys Pro Asp Cys Ile Ile Thr Cys Asp
 35 40 45
 Gly Arg Asn Leu Thr Thr Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln
 50 55 60
 Phe Ser Cys Thr Leu Gly Asp Glu Phe Glu Glu Thr Thr Ala Asp Gly
 65 70 75 80
 Arg Lys Thr Gln Thr Val Cys Asn Phe Thr Asp Gly Ala Leu Val Gln
 85 90 95
 His Gln Glu Trp Asp Gly Lys Glu Ser Thr Ile Thr Arg Lys Leu Lys
 100 105 110
 Asp Gly Lys Leu Val Val Glu Cys Val Met Asn Asn Val Thr Cys Thr
 115 120 125
 Arg Ile Tyr Glu Lys Val Glu
 130 135

<210> 60
 <211> 135
 <212> PRT
 <213> Bos taurus

<400> 60
 Met Ala Thr Val Gln Gln Leu Val Gly Arg Trp Arg Leu Val Glu Ser
 1 5 10 15
 Lys Gly Phe Asp Glu Tyr Met Lys Glu Val Gly Val Gly Met Ala Leu
 20 25 30
 Arg Lys Val Gly Ala Met Ala Lys Pro Asp Cys Ile Ile Thr Ser Asp
 35 40 45
 Gly Lys Asn Leu Ser Ile Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln
 50 55 60

Cura 468 SEQ list 0705

Phe Ser Cys Lys Leu Gly Glu Lys Phe Glu Glu Thr Thr Ala Asp Gly
65 70 75 80
Arg Lys Thr Gln Thr Val Cys Asn Phe Thr Asp Gly Ala Leu Val Gln
85 90 95
His Gln Glu Trp Asp Gly Lys Glu Ser Thr Ile Thr Arg Lys Leu Glu
100 105 110
Asp Gly Lys Leu Val Val Val Cys Val Met Asn Asn Val Thr Cys Thr
115 120 125
Arg Val Tyr Glu Lys Val Glu
130 135

<210> 61
<211> 266
<212> PRT
<213> Homo sapiens

<400> 61
Met Asn Trp Ala Phe Leu Gln Gly Leu Leu Ser Gly Val Asn Lys Tyr
1 5 10 15
Ser Thr Val Leu Ser Arg Ile Trp Leu Ser Val Val Phe Ile Phe Arg
20 25 30
Val Leu Val Tyr Val Val Ala Ala Glu Glu Val Trp Asp Asp Glu Gln
35 40 45
Lys Asp Phe Val Cys Asn Thr Lys Gln Pro Gly Cys Pro Asn Val Cys
50 55 60
Tyr Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln
65 70 75 80
Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala
85 90 95
Tyr Arg Glu Glu Arg Glu Arg Lys His His Leu Lys His Gly Pro Asn
100 105 110
Ala Pro Ser Leu Tyr Asp Asn Leu Ser Lys Lys Arg Gly Gly Leu Trp
115 120 125
Trp Thr Tyr Leu Leu Ser Leu Ile Phe Lys Ala Ala Val Asp Ala Gly
130 135 140
Phe Leu Tyr Ile Phe His Arg Leu Tyr Lys Asp Tyr Asp Met Pro Arg
145 150 155 160
Val Val Ala Cys Ser Val Glu Pro Cys Pro His Thr Val Asp Cys Tyr
165 170 175
Ile Ser Arg Pro Thr Glu Lys Lys Val Phe Thr Tyr Phe Met Val Thr
180 185 190
Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Ser Glu Val Phe Tyr Leu
195 200 205
Val Gly Lys Arg Cys Met Glu Ile Phe Gly Pro Arg His Arg Arg Pro
210 215 220

Cura 468 SEQ list 0705

Arg Cys Arg Glu Cys Leu Pro Asp Thr Cys Pro Pro Tyr Val Leu Ser
 225 230 235 240
 Gln Gly Gly His Pro Glu Asp Gly Asn Ser Val Leu Met Lys Ala Gly
 245 250 255
 Ser Ala Pro Val Asp Ala Gly Gly Tyr Pro
 260 265

<210> 62
 <211> 265
 <212> PRT
 <213> Rattus norvegicus

<400> 62
 Met Asn Trp Gly Phe Leu Gln Gly Ile Leu Ser Gly Val Asn Lys Tyr
 1 5 10 15
 Ser Thr Ala Leu Gly Arg Ile Trp Leu Ser Val Val Phe Ile Phe Arg
 20 25 30
 Val Leu Val Tyr Val Val Ala Ala Glu Glu Val Trp Asp Asp Glu Gln
 35 40 45
 Lys Asp Phe Ile Cys Asn Thr Lys Gln Pro Gly Cys Pro Asn Val Cys
 50 55 60
 Tyr Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln
 65 70 75 80
 Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala
 85 90 95
 Tyr Arg Glu Glu Arg Glu Arg Lys His Arg Leu Lys His Gly Pro Asp
 100 105 110
 Ala Pro Ala Leu Tyr Ser Asn Leu Ser Lys Lys Arg Gly Gly Leu Trp
 115 120 125
 Trp Thr Tyr Leu Leu Ser Leu Ile Phe Lys Ala Ala Val Asp Ser Gly
 130 135 140
 Phe Leu Tyr Ile Phe His Cys Ile Tyr Lys Asp Tyr Asp Met Pro Arg
 145 150 155 160
 Val Val Ala Cys Ser Val Gln Pro Cys Pro His Thr Val Asp Cys Tyr
 165 170 175
 Ile Ser Arg Pro Thr Glu Lys Lys Val Phe Thr Tyr Phe Met Val Val
 180 185 190
 Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Ser Glu Val Ala Tyr Leu
 195 200 205
 Val Gly Lys Arg Cys Met Glu Val Phe Arg Pro Arg Arg Gln Lys Thr
 210 215 220
 Ser Arg Arg His Gln Leu Pro Asp Thr Cys Pro Pro Tyr Val Ile Ser
 225 230 235 240
 Lys Gly His Pro Gln Asp Glu Ser Thr Val Leu Thr Lys Ala Gly Met

245

255

Ala Thr Val Asp Ala Gly Val Tyr Pro
260 265

<210> 63
<211> 266
<212> PRT
<213> Mus musculus

<400> 63

Met Asn Trp Gly Phe Leu Gln Gly Ile Leu Ser Gly Val Asn Lys Tyr
1 5 10 15
Ser Thr Ala Leu Gly Arg Ile Trp Leu Ser Val Val Phe Ile Phe Arg
20 25 30
Val Leu Val Tyr Val Val Ala Ala Glu Glu Val Trp Asp Asp Asp Gln
35 40 45
Lys Asp Phe Ile Cys Asn Thr Lys Gln Pro Gly Cys Pro Asn Val Cys
50 55 60
Tyr Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln
65 70 75 80
Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala
85 90 95
Tyr Arg Glu Glu Arg Glu Arg Lys His Arg Leu Lys His Gly Pro Asn
100 105 110
Ala Pro Ala Leu Tyr Ser Asn Leu Ser Lys Lys Arg Gly Gly Leu Trp
115 120 125
Trp Thr Tyr Leu Leu Ser Leu Ile Phe Lys Ala Ala Val Asp Ser Gly
130 135 140
Phe Leu Tyr Ile Phe His Cys Ile Tyr Lys Asp Tyr Asp Met Pro Arg
145 150 155 160
Val Val Ala Cys Ser Val Thr Pro Cys Pro His Thr Val Asp Cys Tyr
165 170 175
Ile Ala Arg Pro Thr Glu Lys Lys Val Phe Thr Tyr Phe Met Val Val
180 185 190
Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Ser Glu Val Val Tyr Leu
195 200 205
Val Gly Lys Arg Cys Met Glu Val Phe Arg Pro Arg Arg Arg Lys Ala
210 215 220
Ser Arg Arg His Gln Leu Pro Asp Thr Cys Pro Pro Tyr Val Ile Ser
225 230 235 240
Lys Gly Gly His Pro Gln Asp Glu Ser Val Ile Leu Thr Lys Ala Gly
245 250 255
Met Ala Thr Val Asp Ala Gly Val Tyr Pro
260 265

Cura 468 SEQ list 0705

<210> 64
 <211> 273
 <212> PRT
 <213> Homo sapiens

<400> 64

Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys Tyr
 1 5 10 15
 Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe Arg
 20 25 30
 Val Leu Val Tyr Leu Val Thr Ala Glu Arg Val Trp Ser Asp Asp His
 35 40 45
 Lys Asp Phe Asp Cys Asn Thr Arg Gln Pro Gly Cys Ser Asn Val Cys
 50 55 60
 Phe Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln
 65 70 75 80
 Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala
 85 90 95
 Tyr Arg Glu Val Gln Glu Lys Arg His Arg Glu Ala His Gly Glu Asn
 100 105 110
 Ser Gly Arg Leu Tyr Leu Asn Pro Gly Lys Lys Arg Gly Gly Leu Trp
 115 120 125
 Trp Thr Tyr Val Cys Ser Leu Val Phe Lys Ala Ser Val Asp Ile Ala
 130 135 140
 Phe Leu Tyr Val Phe His Ser Phe Tyr Pro Lys Tyr Ile Leu Pro Pro
 145 150 155 160
 Val Val Lys Cys His Ala Asp Pro Cys Pro Asn Ile Val Asp Cys Phe
 165 170 175
 Ile Ser Lys Pro Ser Glu Lys Asn Ile Phe Thr Leu Phe Met Val Ala
 180 185 190
 Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Val Glu Leu Ile Tyr Leu
 195 200 205
 Val Ser Lys Arg Cys His Glu Cys Leu Ala Ala Arg Lys Ala Gln Ala
 210 215 220
 Met Cys Thr Gly His His Pro His Gly Thr Thr Ser Ser Cys Lys Gln
 225 230 235 240
 Asp Asp Leu Leu Ser Gly Asp Leu Ile Phe Leu Gly Ser Asp Ser His
 245 250 255
 Pro Pro Leu Leu Pro Asp Arg Pro Arg Asp His Val Lys Lys Thr Ile
 260 265 270
 Leu

<210> 65

Cura 468 SEQ list 0705

<211> 273

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (41)

<223> wherein Xaa is any amino acid.

<400> 65

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Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys Tyr
 1          5          10          15
Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe Arg
          20          25          30
Val Leu Val Tyr Leu Val Thr Ala Xaa Arg Val Trp Ser Asp Asp His
          35          40          45
Lys Asp Phe Asp Cys Asn Thr Arg Gln Pro Gly Cys Ser Asn Val Cys
          50          55          60
Phe Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln
 65          70          75          80
Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala
          85          90          95
Tyr Arg Glu Val Gln Glu Lys Arg His Arg Glu Ala His Gly Glu Asn
          100          105          110
Ser Gly Arg Leu Tyr Leu Asn Pro Gly Lys Lys Arg Gly Gly Leu Trp
          115          120          125
Trp Thr Tyr Val Cys Ser Leu Val Phe Lys Ala Ser Val Asp Ile Ala
          130          135          140
Phe Leu Tyr Val Phe His Ser Phe Tyr Pro Lys Tyr Ile Leu Pro Pro
145          150          155          160
Val Val Lys Cys His Ala Asp Pro Cys Pro Asn Ile Val Asp Cys Phe
          165          170          175
Ile Ser Lys Pro Ser Glu Lys Asn Ile Phe Thr Leu Phe Met Val Ala
          180          185          190
Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Val Glu Leu Ile Tyr Leu
          195          200          205
Val Ser Lys Arg Cys His Glu Cys Leu Ala Ala Arg Lys Ala Gln Ala
          210          215          220
Met Cys Thr Gly His His Pro His Gly Thr Thr Ser Ser Cys Lys Gln
225          230          235          240
Asp Asp Leu Leu Ser Gly Asp Leu Ile Phe Leu Gly Ser Asp Ser His
          245          250          255
Pro Pro Leu Leu Pro Asp Arg Pro Arg Asp His Val Lys Lys Thr Ile
          260          265          270
Leu

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Cura 468 SEQ list 0705

<210> 66
 <211> 434
 <212> PRT
 <213> Homo sapiens

<400> 66

Ala Lys Gln Gln Leu Asn Leu Arg Thr His Met Ala Asp Glu Asn Lys
 1 5 10 15
 Asn Glu Tyr Ala Ala Gln Leu Gln Asn Phe Asn Gly Glu Gln His Lys
 20 25 30
 His Phe Tyr Val Val Ile Pro Gln Ile Tyr Lys Gln Leu Gln Glu Met
 35 40 45
 Asp Glu Arg Arg Thr Ile Lys Leu Ser Glu Cys Tyr Arg Gly Phe Ala
 50 55 60
 Asp Ser Glu Arg Lys Val Ile Pro Ile Ile Ser Lys Cys Leu Glu Gly
 65 70 75 80
 Met Ile Leu Ala Ala Lys Ser Val Asp Glu Arg Arg Asp Ser Gln Met
 85 90 95
 Val Val Asp Ser Phe Lys Ser Gly Phe Glu Pro Pro Gly Asp Phe Pro
 100 105 110
 Phe Glu Asp Tyr Ser Gln His Ile Tyr Arg Thr Ile Ser Asp Gly Thr
 115 120 125
 Ile Ser Ala Ser Lys Gln Glu Ser Gly Lys Met Asp Ala Lys Thr Thr
 130 135 140
 Val Gly Lys Ala Lys Gly Lys Leu Trp Leu Phe Gly Lys Lys Pro Lys
 145 150 155 160
 Pro Gln Ser Pro Pro Leu Thr Pro Thr Ser Leu Phe Thr Ser Ser Thr
 165 170 175
 Pro Asn Gly Ser Gln Phe Leu Thr Phe Ser Ile Glu Pro Val His Tyr
 180 185 190
 Cys Met Asn Glu Ile Lys Thr Gly Lys Pro Arg Ile Pro Ser Phe Arg
 195 200 205
 Ser Leu Lys Arg Gly Gly Pro Ala Leu Glu Asp Phe Ser His Leu Pro
 210 215 220
 Pro Glu Gln Arg Arg Lys Lys Leu Gln Gln Arg Ile Asp Glu Leu Asn
 225 230 235 240
 Arg Glu Leu Gln Lys Glu Ser Asp Gln Lys Asp Ala Leu Asn Lys Met
 245 250 255
 Lys Asp Val Tyr Glu Lys Asn Pro Gln Met Gly Asp Pro Gly Ser Leu
 260 265 270
 Gln Pro Lys Leu Ala Glu Thr Met Asn Asn Ile Asp Arg Leu Arg Met
 275 280 285
 Glu Ile His Lys Asn Glu Ala Trp Leu Ser Glu Val Glu Gly Lys Thr

Cura 468 SEQ list 0705
300

290

295

Gly Gly Arg Gly Asp Arg Arg His Ser Ser Asp Ile Asn His Leu Val
305 310 315 320
Thr Gln Gly Arg Glu Ser Pro Glu Gly Ser Tyr Thr Asp Asp Ala Asn
325 330 335
Gln Glu Val Arg Gly Pro Pro Gln Gln His Gly His His Asn Glu Phe
340 345 350
Asp Asp Glu Phe Glu Asp Asp Asp Pro Leu Pro Ala Ile Gly His Cys
355 360 365
Lys Ala Ile Tyr Pro Phe Asp Gly His Asn Glu Gly Thr Leu Ala Met
370 375 380
Lys Glu Gly Glu Val Leu Tyr Ile Ile Glu Glu Asp Lys Gly Asp Gly
385 390 395 400
Trp Thr Arg Ala Arg Arg Gln Asn Gly Glu Glu Gly Tyr Val Pro Thr
405 410 415
Ser Tyr Ile Asp Val Thr Leu Glu Lys Asn Ser Lys Gly Ala Val Thr
420 425 430
Tyr Ile

<210> 67
<211> 330
<212> PRT
<213> Homo sapiens

<400> 67

Met Asp Glu Arg Arg Thr Ile Lys Leu Ser Glu Cys Tyr Arg Gly Phe
1 5 10 15
Ala Asp Ser Glu Arg Lys Val Ile Pro Ile Ile Ser Lys Cys Leu Glu
20 25 30
Gly Met Ile Leu Ala Ala Lys Ser Val Asp Glu Arg Arg Asp Ser Gln
35 40 45
Met Val Val Asp Ser Phe Lys Ser Gly Phe Glu Pro Pro Gly Asp Phe
50 55 60
Pro Phe Glu Asp Tyr Ser Gln His Ile Tyr Arg Thr Ile Ser Asp Gly
65 70 75 80
Thr Ile Ser Ala Ser Lys Gln Glu Ser Gly Lys Met Asp Ala Lys Thr
85 90 95
Thr Val Gly Lys Ala Lys Gly Lys Leu Trp Leu Phe Gly Lys Lys Pro
100 105 110
Lys Gly Pro Ala Leu Glu Asp Phe Ser His Leu Pro Pro Glu Gln Arg
115 120 125
Arg Lys Lys Leu Gln Gln Arg Ile Asp Glu Leu Asn Arg Glu Leu Gln
130 135 140

Cura 468 SEQ list 0705

Lys Glu Ser Asp Gln Lys Asp Ala Leu Asn Lys Met Lys Asp Val Tyr
 145 150 155 160
 Glu Lys Asn Pro Gln Met Gly Asp Pro Gly Ser Leu Gln Pro Lys Leu
 165 170 175
 Ala Glu Thr Met Asn Asn Ile Asp Arg Leu Arg Met Glu Ile His Lys
 180 185 190
 Asn Glu Ala Trp Leu Ser Glu Val Glu Gly Lys Thr Gly Gly Arg Gly
 195 200 205
 Asp Arg Arg His Ser Ser Asp Ile Asn His Leu Val Thr Gln Gly Arg
 210 215 220
 Glu Ser Pro Glu Gly Ser Tyr Thr Asp Asp Ala Asn Gln Glu Val Arg
 225 230 235 240
 Gly Pro Pro Gln Gln His Gly His His Asn Glu Phe Asp Asp Glu Phe
 245 250 255
 Glu Asp Asp Asp Pro Leu Pro Ala Ile Gly His Cys Lys Ala Ile Tyr
 260 265 270
 Pro Phe Asp Gly His Asn Glu Gly Thr Leu Ala Met Lys Glu Gly Glu
 275 280 285
 Val Leu Tyr Ile Ile Glu Glu Asp Lys Gly Asp Gly Trp Thr Arg Ala
 290 295 300
 Arg Arg Gln Asn Gly Glu Glu Gly Tyr Val Pro Thr Ser Tyr Ile Asp
 305 310 315 320
 Val Thr Leu Glu Lys Asn Ser Lys Gly Ser
 325 330

<210> 68
 <211> 592
 <212> PRT
 <213> Homo sapiens

<400> 68
 Met Ser Trp Gly Thr Glu Leu Trp Asp Gln Phe Asp Asn Leu Glu Lys
 1 5 10 15
 His Thr Gln Trp Gly Ile Asp Ile Leu Glu Lys Tyr Ile Lys Phe Val
 20 25 30
 Lys Glu Arg Thr Glu Ile Glu Leu Ser Tyr Ala Lys Gln Leu Arg Asn
 35 40 45
 Leu Ser Lys Lys Tyr Gln Pro Lys Lys Asn Ser Lys Glu Glu Glu Glu
 50 55 60
 Tyr Lys Tyr Thr Ser Cys Lys Ala Phe Ile Ser Asn Leu Asn Glu Met
 65 70 75 80
 Asn Asp Tyr Ala Gly Gln His Glu Val Ile Ser Glu Asn Met Ala Ser
 85 90 95
 Gln Ile Ile Val Asp Leu Ala Arg Tyr Val Gln Glu Leu Lys Gln Glu
 100 105 110

Cura 468 SEQ list 0705

Arg Lys Ser Asn Phe His Asp Gly Arg Lys Ala Gln Gln His Ile Glu
 115 120 125
 Thr Cys Trp Lys Gln Leu Glu Ser Ser Lys Arg Arg Phe Glu Arg Asp
 130 135 140
 Cys Lys Glu Ala Asp Arg Ala Gln Gln Tyr Phe Glu Lys Met Asp Ala
 145 150 155 160
 Asp Ile Asn Val Thr Lys Ala Asp Val Glu Lys Ala Arg Gln Gln Ala
 165 170 175
 Gln Ile Arg His Gln Met Ala Glu Asp Ser Lys Ala Asp Tyr Ser Ser
 180 185 190
 Ile Leu Gln Lys Phe Asn His Glu Gln His Glu Tyr Tyr His Thr His
 195 200 205
 Ile Pro Asn Ile Phe Gln Lys Ile Gln Glu Met Glu Glu Arg Arg Ile
 210 215 220
 Val Arg Met Gly Glu Ser Met Lys Thr Tyr Ala Glu Val Asp Arg Gln
 225 230 235 240
 Val Ile Pro Ile Ile Gly Lys Cys Leu Asp Gly Ile Val Lys Ala Ala
 245 250 255
 Glu Ser Ile Asp Gln Lys Asn Asp Ser Gln Leu Val Ile Glu Ala Tyr
 260 265 270
 Lys Ser Gly Phe Glu Pro Pro Gly Asp Ile Glu Phe Glu Asp Tyr Thr
 275 280 285
 Gln Pro Met Lys Arg Thr Val Ser Asp Asn Ser Leu Ser Asn Ser Arg
 290 295 300
 Gly Glu Gly Lys Pro Asp Leu Lys Phe Gly Gly Lys Ser Lys Gly Lys
 305 310 315 320
 Leu Trp Pro Phe Ile Lys Lys Asn Lys Ser Pro Lys Gln Gln Lys Glu
 325 330 335
 Pro Leu Ser His Arg Phe Asn Glu Phe Met Thr Ser Lys Pro Lys Ile
 340 345 350
 His Cys Phe Arg Ser Leu Lys Arg Gly Leu Ser Leu Lys Leu Gly Ala
 355 360 365
 Thr Pro Glu Asp Phe Ser Asn Leu Pro Pro Glu Gln Arg Arg Lys Lys
 370 375 380
 Leu Gln Gln Lys Val Asp Glu Leu Asn Lys Glu Ile Gln Lys Glu Met
 385 390 395 400
 Asp Gln Arg Asp Ala Ile Thr Lys Met Lys Asp Val Tyr Leu Lys Asn
 405 410 415
 Pro Gln Met Gly Asp Pro Ala Ser Leu Asp His Lys Leu Ala Glu Val
 420 425 430
 Ser Gln Asn Ile Glu Lys Leu Arg Val Glu Thr Gln Lys Phe Glu Ala
 435 440 445

Cura 468 SEQ list 0705

Trp Leu Ala Glu Val Glu Gly Arg Leu Pro Ala Arg Asn Glu Gln Ala
450 455 460
Arg Arg Gln Ser Gly Leu Tyr Asp Ser Gln Asn Pro Pro Thr Val Asn
465 470 475 480
Asn Cys Ala Gln Asp Arg Glu Ser Pro Asp Gly Ser Tyr Thr Glu Glu
485 490 495
Gln Ser Gln Glu Ser Glu Met Lys Val Leu Ala Thr Asp Phe Asp Asp
500 505 510
Glu Phe Asp Asp Glu Glu Pro Leu Pro Ala Ile Gly Thr Cys Lys Ala
515 520 525
Leu Tyr Thr Phe Glu Gly Gln Asn Glu Gly Thr Ile Ser Val Val Glu
530 535 540
Gly Glu Thr Leu Tyr Val Ile Glu Glu Asp Lys Gly Asp Gly Trp Thr
545 550 555 560
Arg Ile Arg Arg Asn Glu Asp Glu Glu Gly Tyr Val Pro Thr Ser Tyr
565 570 575
Val Glu Val Cys Leu Asp Lys Asn Ala Lys Gly Ala Lys Thr Tyr Ile
580 585 590

<210> 69
<211> 679
<212> PRT
<213> Homo sapiens

<400> 69
Leu Trp Asn Gly Gly Glu Glu Glu Pro Pro Arg Arg Pro Arg Ala Arg
1 5 10 15
Ser Cys Glu Pro Glu Glu Ala Ala Arg Thr Pro Gly Phe Pro Pro Ser
20 25 30
Arg Gly Ser Arg Gly Ala Lys Gly Ser Pro Gly Arg Gly Thr Arg Glu
35 40 45
Pro Arg Pro Pro Arg Gly Ala Pro Leu Arg Val Pro Cys Thr Met Ser
50 55 60
Trp Gly Thr Glu Leu Trp Asp Gln Phe Asp Asn Leu Glu Lys His Thr
65 70 75 80
Gln Trp Gly Ile Asp Ile Leu Glu Lys Tyr Ile Lys Phe Val Lys Glu
85 90 95
Arg Thr Glu Ile Glu Leu Ser Tyr Ala Lys Gln Leu Arg Asn Leu Ser
100 105 110
Lys Lys Tyr Gln Pro Lys Lys Asn Ser Lys Glu Glu Glu Glu Tyr Lys
115 120 125
Tyr Thr Ser Cys Lys Ala Phe Ile Ser Asn Leu Asn Glu Met Asn Asp

Cura 468 SEQ list 0705

130 135 140
 Tyr Ala Gly Gln His Glu Val Ile Ser Glu Asn Met Ala Ser Gln Ile
 145 150 155 160
 Ile Val Asp Leu Ala Arg Tyr Val Gln Glu Leu Lys Gln Glu Arg Lys
 165 170 175
 Ser Asn Phe His Asp Gly Arg Lys Ala Gln Gln His Ile Glu Thr Cys
 180 185 190
 Trp Lys Gln Leu Glu Ser Ser Lys Arg Arg Phe Glu Arg Asp Cys Lys
 195 200 205
 Glu Ala Asp Arg Ala Gln Gln Tyr Phe Glu Lys Met Asp Ala Asp Ile
 210 215 220
 Asn Val Thr Lys Ala Asp Val Glu Lys Ala Arg Gln Gln Ala Gln Ile
 225 230 235 240
 Arg His Gln Met Ala Glu Asp Ser Lys Ala Asp Tyr Ser Ser Ile Leu
 245 250 255
 Gln Lys Phe Asn His Glu Gln His Glu Tyr Tyr His Thr His Ile Pro
 260 265 270
 Asn Ile Phe Gln Lys Ile Gln Glu Met Glu Glu Arg Arg Ile Val Arg
 275 280 285
 Met Gly Glu Ser Met Lys Thr Tyr Ala Glu Val Asp Arg Gln Val Ile
 290 295 300
 Pro Ile Ile Gly Lys Cys Leu Asp Gly Ile Val Lys Ala Ala Glu Ser
 305 310 315 320
 Ile Asp Gln Lys Asn Asp Ser Gln Leu Val Ile Glu Ala Tyr Lys Ser
 325 330 335
 Gly Phe Glu Pro Pro Gly Asp Ile Glu Phe Glu Asp Tyr Thr Gln Pro
 340 345 350
 Met Lys Arg Thr Val Ser Asp Asn Ser Leu Ser Asn Ser Arg Gly Glu
 355 360 365
 Gly Lys Pro Asp Leu Lys Phe Gly Gly Lys Ser Lys Gly Lys Leu Trp
 370 375 380
 Pro Phe Ile Lys Lys Asn Lys Leu Met Ser Leu Leu Thr Ser Pro His
 385 390 395 400
 Gln Pro Pro Pro Pro Pro Pro Ala Ser Ala Ser Pro Ser Ala Val Pro
 405 410 415
 Asn Gly Pro Gln Ser Pro Lys Gln Gln Lys Glu Pro Leu Ser His Arg
 420 425 430
 Phe Asn Glu Phe Met Thr Ser Lys Pro Lys Ile His Cys Phe Arg Ser
 435 440 445
 Leu Lys Arg Gly Leu Ser Leu Lys Leu Gly Ala Thr Pro Glu Asp Phe
 450 455 460
 Ser Asn Leu Pro Pro Glu Gln Arg Arg Lys Lys Leu Gln Gln Lys Val

Cura 468 SEQ list 0705
475

465 470 480
 Asp Glu Leu Asn Lys Glu Ile Gln Lys Glu Met Asp Gln Arg Asp Ala
 485 490 495
 Ile Thr Lys Met Lys Asp Val Tyr Leu Lys Asn Pro Gln Met Gly Asp
 500 505 510
 Pro Ala Ser Leu Asp His Lys Leu Ala Glu Val Ser Gln Asn Ile Glu
 515 520 525
 Lys Leu Arg Val Glu Thr Gln Lys Phe Glu Ala Trp Leu Ala Glu Val
 530 535 540
 Glu Gly Arg Leu Pro Ala Arg Ser Glu Gln Ala Arg Arg Gln Ser Gly
 545 550 555 560
 Leu Tyr Asp Ser Gln Asn Pro Pro Thr Val Asn Asn Cys Ala Gln Asp
 565 570 575
 Arg Glu Ser Pro Asp Gly Ser Tyr Thr Glu Glu Gln Ser Gln Glu Ser
 580 585 590
 Glu Met Lys Val Leu Ala Thr Asp Phe Asp Asp Glu Phe Asp Asp Glu
 595 600 605
 Glu Pro Leu Pro Ala Ile Gly Thr Cys Lys Ala Leu Tyr Thr Phe Glu
 610 615 620
 Gly Gln Asn Glu Gly Thr Ile Ser Val Val Glu Gly Glu Thr Leu Tyr
 625 630 635 640
 Val Ile Glu Glu Asp Lys Gly Asp Gly Trp Thr Arg Ile Arg Arg Asn
 645 650 655
 Glu Asp Glu Glu Gly Tyr Val Pro Thr Ser Tyr Val Glu Val Cys Leu
 660 665 670
 Asp Lys Asn Ala Lys Asp Ser
 675

<210> 70
 <211> 674
 <212> PRT
 <213> Homo sapiens

<400> 70
 Glu Glu Glu Pro Pro Arg Arg Pro Arg Ala Arg Ser Cys Glu Pro Glu
 1 5 10 15
 Glu Ala Ala Arg Thr Pro Gly Phe Pro Pro Ser Arg Gly Ser Arg Gly
 20 25 30
 Ala Lys Gly Ser Pro Gly Arg Gly Thr Arg Glu Pro Arg Pro Pro Arg
 35 40 45
 Gly Ala Pro Leu Arg Val Pro Cys Thr Met Ser Trp Gly Thr Glu Leu
 50 55 60
 Trp Asp Gln Phe Asp Asn Leu Glu Lys His Thr Gln Trp Gly Ile Asp
 65 70 75 80

Cura 468 SEQ list 0705

Ile Leu Glu Lys Tyr Ile Lys Phe Val Lys Glu Arg Thr Glu Ile Glu
 85 90 95
 Leu Ser Tyr Ala Lys Gln Leu Arg Asn Leu Ser Lys Lys Tyr Gln Pro
 100 105 110
 Lys Lys Asn Ser Lys Glu Glu Glu Glu Tyr Lys Tyr Thr Ser Cys Lys
 115 120 125
 Ala Phe Ile Ser Asn Leu Asn Glu Met Asn Asp Tyr Ala Gly Gln His
 130 135 140
 Glu Val Ile Ser Glu Asn Met Ala Ser Gln Ile Ile Val Asp Leu Ala
 145 150 155 160
 Arg Tyr Val Gln Glu Leu Lys Gln Glu Arg Lys Ser Asn Phe His Asp
 165 170 175
 Gly Arg Lys Ala Gln Gln His Ile Glu Thr Cys Trp Lys Gln Leu Glu
 180 185 190
 Ser Ser Lys Arg Arg Phe Glu Arg Asp Cys Lys Glu Ala Asp Arg Ala
 195 200 205
 Gln Gln Tyr Phe Glu Lys Met Asp Ala Asp Ile Asn Val Thr Lys Ala
 210 215 220
 Asp Val Glu Lys Ala Arg Gln Gln Ala Gln Ile Arg His Gln Met Ala
 225 230 235 240
 Glu Asp Ser Lys Ala Asp Tyr Ser Ser Ile Leu Gln Lys Phe Asn His
 245 250 255
 Glu Gln His Glu Tyr Tyr His Thr His Ile Pro Asn Ile Phe Gln Lys
 260 265 270
 Ile Gln Glu Met Glu Glu Arg Arg Ile Val Arg Met Gly Glu Ser Met
 275 280 285
 Lys Thr Tyr Ala Glu Val Asp Arg Gln Val Ile Pro Ile Ile Gly Lys
 290 295 300
 Cys Leu Asp Gly Ile Val Lys Ala Ala Glu Ser Ile Asp Gln Lys Asn
 305 310 315 320
 Asp Ser Gln Leu Val Ile Glu Ala Tyr Lys Ser Gly Phe Glu Pro Pro
 325 330 335
 Gly Asp Ile Glu Phe Glu Asp Tyr Thr Gln Pro Met Lys Arg Thr Val
 340 345 350
 Ser Asp Asn Ser Leu Ser Asn Ser Arg Gly Glu Gly Lys Pro Asp Leu
 355 360 365
 Lys Phe Gly Gly Lys Ser Lys Gly Lys Leu Trp Pro Phe Ile Lys Lys
 370 375 380
 Asn Lys Leu Met Ser Leu Leu Thr Ser Pro His Gln Pro Pro Pro Pro
 385 390 395 400
 Pro Pro Ala Ser Ala Ser Pro Ser Ala Val Pro Asn Gly Pro Gln Ser
 405 410 415

Cura 468 SEQ list 0705

Pro Lys Gln Gln Lys Glu Pro Leu Ser His Arg Phe Asn Glu Phe Met
420 425 430

Thr Ser Lys Pro Lys Ile His Cys Phe Arg Ser Leu Lys Arg Gly Leu
435 440 445

Ser Leu Lys Leu Gly Ala Thr Pro Glu Asp Phe Ser Asn Leu Pro Pro
450 455 460

Glu Gln Arg Arg Lys Lys Leu Gln Gln Lys Val Asp Glu Leu Asn Lys
465 470 475 480

Glu Ile Gln Lys Glu Met Asp Gln Arg Asp Ala Ile Thr Lys Met Lys
485 490 495

Asp Val Tyr Leu Lys Asn Pro Gln Met Gly Asp Pro Ala Ser Leu Asp
500 505 510

His Lys Leu Ala Glu Val Ser Gln Asn Ile Glu Lys Leu Arg Val Glu
515 520 525

Thr Gln Lys Phe Glu Ala Trp Leu Ala Glu Val Glu Gly Arg Leu Pro
530 535 540

Ala Arg Ser Glu Gln Ala Arg Arg Gln Ser Gly Leu Tyr Asp Ser Gln
545 550 555 560

Asn Pro Pro Thr Val Asn Asn Cys Ala Gln Asp Arg Glu Ser Pro Asp
565 570 575

Gly Ser Tyr Thr Glu Glu Gln Ser Gln Glu Ser Glu Met Lys Val Leu
580 585 590

Ala Thr Asp Phe Asp Asp Glu Phe Asp Asp Glu Glu Pro Leu Pro Ala
595 600 605

Ile Gly Thr Cys Lys Ala Leu Tyr Thr Phe Glu Gly Gln Asn Glu Gly
610 615 620

Thr Ile Ser Val Val Glu Gly Glu Thr Leu Tyr Val Ile Glu Glu Asp
625 630 635 640

Lys Gly Asp Gly Trp Thr Arg Ile Arg Arg Asn Glu Asp Glu Glu Gly
645 650 655

Tyr Val Pro Thr Ser Tyr Val Glu Val Cys Leu Asp Lys Asn Ala Lys
660 665 670

Asp Ser

<210> 71
<211> 457
<212> PRT
<213> Homo sapiens

<400> 71
Met Ser Leu Met Leu Asp Asp Gln Pro Pro Met Glu Ala Gln Tyr Ala
1 5 10 15
Glu Glu Gly Pro Gly Pro Gly Ile Phe Arg Ala Glu Pro Gly Asp Gln
20 25 30

Cura 468 SEQ list 0705

Gln His Pro Ile Ser Gln Ala Val Cys Trp Arg Ser Met Arg Arg Gly
 35 40 45
 Cys Ala Val Leu Gly Ala Leu Gly Leu Leu Ala Gly Ala Gly Val Gly
 50 55 60
 Ser Trp Leu Leu Val Leu Tyr Leu Cys Pro Ala Ala Ser Gln Pro Ile
 65 70 75 80
 Ser Gly Thr Leu Gln Asp Glu Glu Ile Thr Leu Ser Cys Ser Glu Ala
 85 90 95
 Ser Ala Glu Glu Ala Leu Leu Pro Ala Leu Pro Lys Thr Val Ser Phe
 100 105 110
 Arg Ile Asn Ser Glu Asp Phe Leu Leu Glu Ala Gln Val Arg Asp Gln
 115 120 125
 Pro Arg Trp Leu Leu Val Cys His Glu Gly Trp Ser Pro Ala Leu Gly
 130 135 140
 Leu Gln Ile Cys Trp Ser Leu Gly His Leu Arg Leu Thr His His Lys
 145 150 155 160
 Gly Val Asn Leu Thr Asp Ile Lys Leu Asn Ser Ser Gln Glu Phe Ala
 165 170 175
 Gln Leu Ser Pro Arg Leu Gly Gly Phe Leu Glu Glu Ala Trp Gln Pro
 180 185 190
 Arg Asn Asn Cys Thr Ser Gly Gln Val Val Ser Leu Arg Cys Ser Glu
 195 200 205
 Cys Gly Ala Arg Pro Leu Ala Ser Arg Ile Val Gly Gly Gln Ser Val
 210 215 220
 Ala Pro Gly Arg Trp Pro Trp Gln Ala Ser Val Ala Leu Gly Phe Arg
 225 230 235 240
 His Thr Cys Gly Gly Ser Val Leu Ala Pro Arg Trp Val Val Thr Ala
 245 250 255
 Ala His Cys Met His Ser Phe Arg Leu Ala Arg Leu Ser Ser Trp Arg
 260 265 270
 Val His Ala Gly Leu Val Ser His Ser Ala Val Arg Pro His Gln Gly
 275 280 285
 Ala Leu Val Glu Arg Ile Ile Pro His Pro Leu Tyr Ser Ala Gln Asn
 290 295 300
 His Asp Tyr Asp Val Ala Leu Leu Arg Leu Gln Thr Ala Leu Asn Phe
 305 310 315 320
 Ser Asp Thr Val Gly Ala Val Cys Leu Pro Ala Lys Glu Gln His Phe
 325 330 335
 Pro Lys Gly Ser Arg Cys Trp Val Ser Gly Trp Gly His Thr His Pro
 340 345 350
 Ser His Thr Tyr Ser Ser Asp Met Leu Gln Asp Thr Val Val Pro Leu
 355 360 365

Cura 468 SEQ list 0705

Phe Ser Thr Gln Leu Cys Asn Ser Ser Cys Val Tyr Ser Gly Ala Leu
 370 375 380
 Thr Pro Arg Met Leu Cys Ala Gly Tyr Leu Asp Gly Arg Ala Asp Ala
 385 390 395 400
 Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Pro Asp Gly Asp Thr
 405 410 415
 Trp Arg Leu Val Gly Val Val Ser Trp Gly Arg Ala Cys Ala Glu Pro
 420 425 430
 Asn His Pro Gly Val Tyr Ala Lys Val Ala Glu Phe Leu Asp Trp Ile
 435 440 445
 His Asp Thr Ala Gln Asp Ser Leu Leu
 450 455

<210> 72
 <211> 455
 <212> PRT
 <213> Mus musculus

<400> 72
 Met Ser Pro Thr Leu Asp Asp Gln Ser Pro Met Glu Ile Arg Cys Thr
 1 5 10 15
 Glu Glu Gly Ala Gly Pro Gly Ile Phe Arg Met Glu Leu Gly Asp Gln
 20 25 30
 Arg Gln Ser Ile Ser Gln Ser Gln Arg Trp Cys Cys Leu Gln Arg Gly
 35 40 45
 Cys Val Ile Leu Gly Val Leu Gly Leu Leu Ala Gly Ala Gly Ile Ala
 50 55 60
 Ser Trp Leu Leu Val Leu Tyr Leu Trp Pro Ala Ala Ser Pro Ser Ile
 65 70 75 80
 Ser Gly Thr Leu Gln Glu Glu Glu Met Thr Leu Asn Cys Pro Gly Val
 85 90 95
 Ser Cys Glu Glu Glu Leu Leu Pro Ser Leu Pro Lys Thr Val Ser Phe
 100 105 110
 Arg Ile Asn Gly Glu Asp Leu Leu Gln Val Gln Val Arg Ala Arg
 115 120 125
 Pro Asp Trp Leu Leu Val Cys His Glu Gly Trp Ser Pro Ala Leu Gly
 130 135 140
 Met His Ile Cys Lys Ser Leu Gly His Ile Arg Leu Thr Gln His Lys
 145 150 155 160
 Ala Val Asn Leu Ser Asp Ile Lys Leu Asn Arg Ser Gln Glu Phe Ala
 165 170 175
 Gln Leu Ser Ala Arg Pro Gly Gly Leu Val Glu Glu Ala Trp Lys Pro
 180 185 190
 Ser Ala Asn Cys Pro Ser Gly Arg Ile Val Ser Leu Lys Cys Ser Glu

Cura 468 SEQ list 0705

195

200

205

Cys Gly Ala Arg Pro Leu Ala Ser Arg Ile Val Gly Gly Gln Ala Val
 210 215 220
 Ala Ser Gly Arg Trp Pro Trp Gln Ala Ser Val Met Leu Gly Ser Arg
 225 230 235 240
 His Thr Cys Gly Ala Ser Val Leu Ala Pro His Trp Val Val Thr Ala
 245 250 255
 Ala His Cys Met Tyr Ser Phe Arg Leu Ser Arg Leu Ser Ser Trp Arg
 260 265 270
 Val His Ala Gly Leu Val Ser His Gly Ala Val Arg Gln His Gln Gly
 275 280 285
 Thr Met Val Glu Lys Ile Ile Pro His Pro Leu Tyr Ser Ala Gln Asn
 290 295 300
 His Asp Tyr Asp Val Ala Leu Leu Gln Leu Arg Thr Pro Ile Asn Phe
 305 310 315 320
 Ser Asp Thr Val Asp Ala Val Cys Leu Pro Ala Lys Glu Gln Tyr Phe
 325 330 335
 Pro Trp Gly Ser Gln Cys Trp Val Ser Gly Trp Gly His Thr Asp Pro
 340 345 350
 Ser His Thr His Ser Ser Asp Thr Leu Gln Asp Thr Met Val Pro Leu
 355 360 365
 Leu Ser Thr His Leu Cys Asn Ser Ser Cys Met Tyr Ser Gly Ala Leu
 370 375 380
 Thr His Arg Met Leu Cys Ala Gly Tyr Leu Asp Gly Arg Ala Asp Ala
 385 390 395 400
 Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Pro Ser Gly Asp Thr
 405 410 415
 Trp His Leu Val Gly Val Val Ser Trp Gly Arg Gly Cys Ala Glu Pro
 420 425 430
 Asn Arg Pro Gly Val Tyr Ala Lys Val Ala Glu Phe Leu Asp Trp Ile
 435 440 445
 His Asp Thr Val Gln Val Arg
 450 455

<210> 73

<211> 445

<212> PRT

<213> Mus musculus

<400> 73

Met Glu Ile Arg Cys Thr Glu Glu Gly Ala Gly Pro Gly Ile Phe Arg
 1 5 10 15

Met Glu Leu Gly Asp Gln Arg Gln Ser Ile Ser Gln Ser Gln Arg Trp
 20 25 30

Cura 468 SEQ list 0705

Cys Cys Leu Gln Arg Gly Cys Val Ile Leu Gly Val Leu Gly Leu Leu
 35 40 45
 Ala Gly Ala Gly Ile Ala Ser Trp Leu Leu Val Leu Tyr Leu Trp Pro
 50 55 60
 Ala Ala Ser Pro Ser Ile Ser Gly Thr Leu Gln Glu Glu Glu Met Thr
 65 70 75 80
 Leu Asn Cys Pro Gly Val Ser Cys Glu Glu Glu Leu Leu Pro Ser Leu
 85 90 95
 Pro Lys Thr Val Ser Phe Arg Ile Asn Gly Glu Asp Leu Leu Leu Gln
 100 105 110
 Val Gln Val Arg Ala Arg Pro Asp Trp Leu Leu Val Cys His Glu Gly
 115 120 125
 Trp Ser Pro Ala Leu Gly Met His Ile Cys Lys Ser Leu Gly His Ile
 130 135 140
 Arg Leu Thr Gln His Lys Ala Val Asn Leu Ser Asp Ile Lys Leu Asn
 145 150 155 160
 Arg Ser Gln Glu Phe Ala Gln Leu Ser Ala Arg Pro Gly Gly Leu Val
 165 170 175
 Glu Glu Ala Trp Lys Pro Ser Ala Asn Cys Pro Ser Gly Arg Ile Val
 180 185 190
 Ser Leu Lys Cys Ser Glu Cys Gly Ala Arg Pro Leu Ala Ser Arg Ile
 195 200 205
 Val Gly Gly Gln Ala Val Ala Ser Gly Arg Trp Pro Trp Gln Ala Ser
 210 215 220
 Val Met Leu Gly Ser Arg His Thr Cys Gly Ala Ser Val Leu Ala Pro
 225 230 235 240
 His Trp Val Val Thr Ala Ala His Cys Met Tyr Ser Phe Arg Leu Ser
 245 250 255
 Arg Leu Ser Ser Trp Arg Val His Ala Gly Leu Val Ser His Gly Ala
 260 265 270
 Val Arg Gln His Gln Gly Thr Met Val Glu Lys Ile Ile Pro His Pro
 275 280 285
 Leu Tyr Ser Ala Gln Asn His Asp Tyr Asp Val Ala Leu Leu Gln Leu
 290 295 300
 Arg Thr Pro Ile Asn Phe Ser Asp Thr Val Gly Ala Val Cys Leu Pro
 305 310 315 320
 Ala Lys Glu Gln Tyr Phe Pro Trp Gly Ser Gln Cys Trp Val Ser Gly
 325 330 335
 Trp Gly His Thr Asp Pro Ser His Thr His Ser Ser Asp Thr Leu Gln
 340 345 350
 Asp Thr Met Val Pro Leu Leu Ser Thr His Leu Cys Asn Ser Ser Cys
 355 360 365

Cura 468 SEQ list 0705

Met Tyr Ser Gly Ala Leu Thr His Arg Met Leu Cys Ala Gly Tyr Leu
 370 375 380
 Asp Gly Arg Ala Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val
 385 390 395 400
 Cys Pro Ser Gly Asp Thr Trp His Leu Val Gly Val Val Ser Trp Gly
 405 410 415
 Arg Gly Cys Ala Glu Pro Asn Arg Pro Gly Val Tyr Ala Lys Val Ala
 420 425 430
 Glu Phe Leu Asp Trp Ile His Asp Thr Val Gln Val Arg
 435 440 445

<210> 74
 <211> 398
 <212> PRT
 <213> Homo sapiens

<400> 74
 Met Ser Leu Met Leu Asp Asp Gln Pro Pro Met Glu Ala Gln Tyr Ala
 1 5 10 15
 Glu Glu Gly Pro Gly Pro Gly Ile Phe Arg Ala Glu Pro Gly Asp Gln
 20 25 30
 Gln His Pro Ile Ser Gln Ala Val Cys Trp Arg Ser Met Arg Arg Gly
 35 40 45
 Cys Ala Val Leu Gly Ala Leu Gly Leu Leu Ala Gly Ala Gly Val Gly
 50 55 60
 Ser Trp Leu Leu Val Leu Tyr Leu Cys Pro Ala Ala Ser Gln Pro Ile
 65 70 75 80
 Ser Gly Thr Leu Gln Asp Glu Glu Ile Thr Leu Ser Cys Ser Glu Ala
 85 90 95
 Ser Ala Glu Glu Ala Leu Leu Pro Ala Leu Pro Lys Thr Val Ser Phe
 100 105 110
 Arg Ile Asn Ser Glu Asp Phe Leu Leu Glu Ala Gln Val Arg Asp Gln
 115 120 125
 Pro Arg Trp Leu Leu Val Cys His Glu Gly Trp Ser Pro Ala Leu Gly
 130 135 140
 Leu Gln Ile Cys Trp Ser Leu Gly His Leu Arg Leu Thr His His Lys
 145 150 155 160
 Gly Val Asn Leu Thr Asp Ile Lys Leu Asn Ser Ser Gln Glu Phe Ala
 165 170 175
 Gln Leu Ser Pro Arg Leu Gly Gly Phe Leu Glu Glu Ala Trp Gln Pro
 180 185 190
 Arg Asn Asn Cys Thr Ser Gly Gln Val Val Ser Leu Arg Cys Ser Glu
 195 200 205
 Cys Gly Ala Arg Pro Leu Ala Ser Arg Ile Val Gly Gly Gln Ser Val
 210 215 220

Cura 468 SEQ list 0705

Ala Pro Gly Arg Trp Pro Trp Gln Ala Ser Val Ala Leu Gly Phe Arg
 225 230 235 240
 His Thr Cys Gly Gly Ser Val Leu Ala Pro Arg Trp Val Val Thr Ala
 245 250 255
 Ala His Cys Met His Ser Phe Arg Leu Ala Arg Leu Ser Ser Trp Arg
 260 265 270
 Val His Ala Gly Leu Val Ser His Ser Ala Val Arg Pro His Gln Gly
 275 280 285
 Ala Leu Val Glu Arg Ile Ile Pro His Pro Leu Tyr Ser Ala Gln Asn
 290 295 300
 His Asp Tyr Asp Val Ala Leu Leu Arg Leu Gln Thr Ala Leu Asn Phe
 305 310 315 320
 Ser Asp Thr Val Gly Ala Val Cys Leu Pro Ala Lys Glu Gln His Phe
 325 330 335
 Pro Lys Gly Ser Arg Cys Trp Val Ser Gly Trp Gly His Thr His Pro
 340 345 350
 Ser His Ser Leu Gln Leu Gly Tyr Ala Pro Gly His Gly Gly Ala Leu
 355 360 365
 Val Gln His Ser Ala Leu Gln Gln Leu Leu Arg Val Gln Arg Ser Pro
 370 375 380
 His Pro Pro His Ala Leu Arg Trp Leu Pro Gly Arg Lys Gly
 385 390 395

<210> 75
 <211> 311
 <212> PRT
 <213> Mus musculus

<400> 75
 Met His Ile Cys Lys Ser Leu Gly His Ile Arg Leu Thr Gln His Lys
 1 5 10 15
 Ala Val Asn Leu Ser Asp Ile Lys Leu Asn Arg Ser Gln Glu Phe Ala
 20 25 30
 Gln Leu Ser Ala Arg Pro Gly Gly Leu Val Glu Glu Ala Trp Lys Pro
 35 40 45
 Ser Ala Asn Cys Pro Ser Gly Arg Ile Val Ser Leu Lys Cys Ser Glu
 50 55 60
 Cys Gly Ala Arg Pro Leu Ala Ser Arg Ile Val Gly Gly Gln Ala Val
 65 70 75 80
 Ala Ser Gly Arg Trp Pro Trp Gln Ala Ser Val Met Leu Gly Ser Arg
 85 90 95
 His Thr Cys Gly Ala Ser Val Leu Ala Pro His Trp Val Val Thr Ala
 100 105 110
 Ala His Cys Met Tyr Ser Phe Arg Leu Ser Arg Leu Ser Ser Trp Arg

125

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<210> 76
<211> 199
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Reprolysin
      family zinc protease Consensus Sequence

<400> 76
Lys Tyr Ile Glu Leu Phe Ile Val Val Asp His Gly Met Phe Thr Lys
 1          5          10          15
Tyr Gly Ser Asp Leu Asn Lys Ile Arg Gln Arg Val His Gln Ile Val
          20          25          30
Asn Leu Val Asn Glu Ile Tyr Arg Pro Leu Asn Ile Arg Val Val Leu
          35          40          45
Val Gly Leu Glu Ile Trp Ser Asp Gly Asp Lys Ile Thr Val Gln Gly
          50          55          60
Asp Ala Asn Asp Thr Leu His Arg Phe Leu Glu Trp Arg Glu Thr Asp
 65          70          75          80

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Cura 468 SEQ list 0705

Leu Leu Lys Arg Lys Ser His Asp Asn Ala Gln Leu Leu Thr Gly Ile
85 90 95
Asp Phe Asp Gly Asn Thr Ile Gly Ala Ala Tyr Val Gly Gly Met Cys
100 105 110
Ser Pro Lys Arg Ser Val Gly Val Val Gln Asp His Ser Pro Ile Val
115 120 125
Leu Leu Val Ala Val Thr Met Ala His Glu Leu Gly His Asn Leu Gly
130 135 140
Met Thr His Asp Asp Ile Asn Lys Cys Thr Cys Glu Gly Gly Gly Gly
145 150 155 160
Cys Ile Met Asn Pro Val Ala Ser Ser Ser Pro Gly Lys Lys Phe Ser
165 170 175
Asn Cys Ser Met Asp Asp Tyr Gln Gln Phe Leu Thr Lys Gly Lys Pro
180 185 190
Gln Cys Leu Leu Asn Lys Pro
195

<210> 77
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Thrombospondin
type 1 Consensus Sequence

<400> 77
Trp Gly Glu Trp Ser Glu Trp Ser Pro Cys Ser Val Thr Cys Gly Gly
1 5 10 15
Gly Val Gln Thr Arg Thr Arg Cys Cys Asn Pro Pro Pro Asn Gly Gly
20 25 30
Gly Pro Cys Thr Gly Pro Asp Thr Glu Thr Arg Ala Cys Asn Glu Gln
35 40 45
Pro Cys Pro
50

<210> 78
<211> 48
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Thrombospondin
type 1 domain Consensus Sequence

<400> 78
Ser Pro Trp Ser Glu Trp Ser Pro Cys Ser Val Thr Cys Gly Lys Gly
1 5 10 15
Ile Arg Thr Arg Gln Arg Thr Cys Asn Ser Pro Ala Gly Gly Lys Pro

20

Cys Thr Gly Asp Ala Gln Glu Thr Glu Ala Cys Met Met Asp Pro Cys
35 40 45

<210> 79

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Reprolysin
family propeptide Consensus Sequence

<400> 79

His Leu Glu Lys Asn Arg Ser Leu Leu Ala Pro Asp Phe Thr Val Thr
1 5 10 15
Thr Tyr Asp Asp Asp Gly Thr Leu Val Thr Glu His Pro Leu Ile Gln
20 25 30
Asp His Cys Tyr Tyr Gln Gly Tyr Val Glu Gly Tyr Pro Asn Ser Ala
35 40 45
Val Ser Leu Ser Thr Cys Ser Gly Leu Arg Gly Ile Leu Gln Leu Glu
50 55 60
Asn Leu Ser Tyr Gly Ile Glu Pro Leu Glu Ser Ser Asp Gly Phe Glu
65 70 75 80
His Ile Ile Tyr Gln Ile Glu His Leu Lys Thr Val Pro Gly Pro Cys
85 90 95
Gly Glu Cys Gly Ser Leu Ser Val Ser Thr Asp Ser Gln Tyr Gly Ile
100 105 110
Arg Ser Pro Ser Pro
115

<210> 80

<211> 751

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Alpha-2-macroglobulin family Consensus Sequence

<400> 80

Ile Asp Glu Asp Asp Ile Thr Ile Arg Ser Tyr Phe Pro Glu Ser Trp
1 5 10 15
Leu Trp Glu Val Glu Glu Val Asp Arg Ser Pro Val Leu Thr Val Asn
20 25 30
Ile Thr Leu Pro Asp Ser Ile Thr Thr Trp Glu Ile Leu Ala Val Ser
35 40 45

Cura 468 SEQ list 0705

Leu Ser Asn Thr Lys Gly Leu Cys Val Ala Asp Pro Val Glu Leu Thr
 50 55 60
 Val Phe Gln Asp Phe Phe Leu Glu Leu Arg Leu Pro Tyr Ser Val Val
 65 70 75 80
 Arg Gly Glu Gln Val Glu Leu Arg Ala Val Leu Tyr Asn Tyr Leu Pro
 85 90 95
 Ser Gln Asp Ile Lys Val Val Val Gln Leu Glu Val Glu Pro Leu Cys
 100 105 110
 Gln Ala Gly Phe Cys Ser Leu Ala Thr Gln Arg Thr Arg Ser Ser Gln
 115 120 125
 Ser Val Arg Pro Lys Ser Leu Ser Ser Val Ser Phe Pro Val Val Val
 130 135 140
 Val Pro Leu Ala Ser Gly Leu Ser Leu Val Glu Val Val Ala Ser Val
 145 150 155 160
 Pro Glu Phe Phe Val Lys Asp Ala Val Val Lys Thr Leu Lys Val Glu
 165 170 175
 Pro Glu Gly Ala Arg Lys Glu Glu Thr Val Ser Ser Leu Leu Leu Pro
 180 185 190
 Pro Glu His Leu Gly Gly Gly Leu Glu Val Ser Glu Val Pro Ala Leu
 195 200 205
 Lys Leu Pro Asp Asp Val Pro Asp Thr Glu Ala Glu Ala Val Ile Ser
 210 215 220
 Val Gln Gly Asp Pro Val Ala Gln Ala Ile Gln Asn Thr Leu Ser Gly
 225 230 235 240
 Glu Gly Leu Asn Asn Leu Leu Arg Leu Pro Ser Gly Cys Gly Glu Gln
 245 250 255
 Asn Met Ile Tyr Met Ala Pro Thr Val Tyr Val Leu His Tyr Leu Asp
 260 265 270
 Glu Thr Trp Gln Trp Glu Lys Pro Gly Thr Lys Lys Lys Gln Lys Ala
 275 280 285
 Ile Asp Leu Ile Asn Lys Gly Tyr Gln Arg Gln Leu Asn Tyr Arg Lys
 290 295 300
 Ala Asp Gly Ser Tyr Ala Ala Phe Leu His Arg Ala Ser Ser Thr Trp
 305 310 315 320
 Leu Thr Ala Phe Val Leu Lys Val Phe Ser Gln Ala Arg Asn Tyr Val
 325 330 335
 Phe Ile Asp Glu Glu His Ile Cys Gly Ala Val Lys Trp Leu Ile Leu
 340 345 350
 Asn Gln Gln Lys Asp Asp Gly Val Phe Arg Glu Ser Gly Pro Val Ile
 355 360 365
 His Asn Glu Met Lys Gly Gly Val Gly Asp Asp Ala Glu Val Glu Val
 370 375 380

Cura 468 SEQ list 0705

Thr Leu Thr Ala Phe Ile Thr Ile Ala Leu Leu Glu Ala Lys Leu Val
385 390 395 400

Cys Ile Ser Pro Val Val Ala Asn Ala Leu Ser Ile Leu Lys Ala Ser
405 410 415

Asp Tyr Leu Leu Glu Asn Tyr Ala Asn Gly Gln Arg Val Tyr Thr Leu
420 425 430

Ala Leu Thr Ala Tyr Ala Leu Ala Leu Ala Gly Val Leu His Lys Leu
435 440 445

Lys Glu Ile Leu Lys Ser Leu Lys Glu Glu Leu Tyr Lys Ala Leu Val
450 455 460

Lys Gly His Trp Glu Arg Pro Gln Lys Pro Lys Asp Ala Pro Gly His
465 470 475 480

Pro Tyr Ser Pro Gln Pro Gln Ala Ala Ala Val Glu Met Thr Ser Tyr
485 490 495

Ala Leu Leu Ala Leu Leu Thr Leu Leu Pro Phe Pro Lys Val Glu Met
500 505 510

Ala Pro Lys Val Val Lys Trp Leu Thr Glu Gln Gln Tyr Tyr Gly Gly
515 520 525

Gly Phe Gly Ser Thr Gln Asp Thr Val Met Ala Leu Gln Ala Leu Ser
530 535 540

Lys Tyr Gly Ile Ala Thr Pro Thr His Lys Glu Lys Asn Leu Ser Val
545 550 555 560

Thr Ile Gln Ser Pro Ser Gly Ser Phe Lys Ser His Phe Gln Ile Leu
565 570 575

Asn Asn Asn Ala Phe Leu Leu Arg Pro Val Glu Leu Pro Leu Asn Glu
580 585 590

Gly Phe Thr Val Thr Ala Lys Val Thr Gly Gln Gly Thr Leu Thr Leu
595 600 605

Val Thr Thr Tyr Arg Tyr Lys Val Leu Asp Lys Lys Asn Thr Phe Cys
610 615 620

Phe Asp Leu Lys Ile Glu Thr Val Pro Asp Thr Cys Val Glu Pro Lys
625 630 635 640

Gly Ala Lys Asn Ser Asp Tyr Leu Ser Ile Cys Thr Arg Tyr Ala Gly
645 650 655

Ser Arg Ser Asp Ser Gly Met Ala Ile Ala Asp Ile Ser Met Leu Thr
660 665 670

Gly Phe Ile Pro Leu Lys Pro Asp Leu Lys Lys Leu Glu Asn Gly Val
675 680 685

Asp Arg Tyr Val Ser Lys Tyr Glu Ile Asp Gly Asn His Val Leu Leu
690 695 700

Tyr Leu Asp Lys Val Ser His Ser Glu Thr Glu Cys Val Gly Phe Lys
705 710 715 720

Cura 468 SEQ list 0705

Ile His Gln Asp Phe Glu Val Gly Leu Leu Gln Pro Ala Ser Val Lys
725 730 735

Val Tyr Asp Tyr Tyr Glu Pro Asp Glu Gln Cys Thr Ala Phe Tyr
740 745 750

<210> 81

<211> 620

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Alpha-2-macroglobulin family N-terminal region

Consensus Sequence

<400> 81

Arg Leu Leu Trp Leu Leu Leu Leu Leu Leu Phe Phe Asp Ser Ser
1 5 10 15

Leu Gln Lys Pro Arg Tyr Met Val Ile Val Pro Ser Ile Leu Arg Thr
20 25 30

Glu Thr Pro Glu Lys Val Cys Val Gln Leu His Asp Leu Asn Glu Thr
35 40 45

Val Thr Val Thr Val Ser Leu His Ser Phe Pro Gly Lys Arg Asn Leu
50 55 60

Ser Ser Leu Phe Thr Val Leu Leu Ser Ser Lys Asp Leu Phe His Cys
65 70 75 80

Val Ser Phe Thr Val Pro Gln Pro Gly Leu Phe Lys Ser Ser Lys Gly
85 90 95

Glu Glu Ser Phe Val Val Val Gln Val Lys Gly Pro Thr His Thr Phe
100 105 110

Lys Glu Lys Val Thr Val Leu Val Ser Ser Arg Arg Gly Leu Val Phe
115 120 125

Ile Gln Thr Asp Lys Pro Ile Tyr Thr Pro Gly Gln Thr Val Arg Tyr
130 135 140

Arg Val Phe Ser Val Asp Glu Asn Leu Arg Pro Leu Asn Glu Leu Ile
145 150 155 160

Leu Val Tyr Ile Glu Asp Pro Glu Gly Asn Arg Val Asp Gln Trp Glu
165 170 175

Val Asn Lys Leu Glu Gly Gly Ile Phe Gln Leu Ser Phe Pro Ile Pro
180 185 190

Ser Glu Pro Ile Gln Gly Thr Trp Lys Ile Val Ala Arg Tyr Glu Ser
195 200 205

Gly Pro Glu Ser Asn Tyr Thr His Tyr Phe Glu Val Lys Glu Tyr Val
210 215 220

Leu Pro Ser Phe Glu Val Ser Ile Thr Pro Pro Lys Pro Phe Ile Tyr
225 230 235 240

Cura 468 SEQ list 0705

Tyr Asp Asn Phe Lys Glu Phe Glu Val Thr Ile Cys Ala Arg Tyr Thr
245 250 255

Tyr Gly Lys Pro Val Pro Gly Val Ala Tyr Val Arg Phe Gly Val Lys
260 265 270

Asp Glu Asp Gly Lys Lys Glu Leu Leu Ala Gly Leu Glu Glu Arg Ala
275 280 285

Lys Leu Leu Asp Gly Asn Gly Glu Ile Cys Leu Ser Gln Glu Val Leu
290 295 300

Leu Lys Glu Leu Gln Leu Lys Asn Glu Asp Leu Glu Gly Lys Ser Leu
305 310 315 320

Tyr Val Ala Val Ala Val Ile Glu Ser Glu Gly Gly Asp Met Glu Glu
325 330 335

Ala Glu Leu Gly Gly Ile Lys Ile Val Arg Ser Pro Tyr Lys Leu Lys
340 345 350

Phe Val Lys Thr Pro Ser His Phe Lys Pro Gly Ile Pro Phe Phe Leu
355 360 365

Lys Val Leu Val Val Asp Pro Asp Gly Ser Pro Ala Pro Asn Val Pro
370 375 380

Val Lys Val Ser Ala Gln Asp Ala Ser Tyr Tyr Ser Asn Gly Thr Thr
385 390 395 400

Asp Glu Asp Gly Leu Ala Gln Phe Ser Ile Asn Thr Ser Gly Ile Ser
405 410 415

Ser Leu Ser Ile Thr Val Arg Thr Asn His Lys Glu Leu Pro Glu Glu
420 425 430

Val Gln Ala His Ala Glu Ala Gln Ala Thr Ala Tyr Ser Thr Val Ser
435 440 445

Leu Ser Lys Ser Tyr Ile His Leu Ser Ile Glu Arg Thr Leu Pro Cys
450 455 460

Gly Pro Gly Val Gly Glu Gln Ala Asn Phe Ile Leu Arg Gly Lys Ser
465 470 475 480

Leu Gly Glu Leu Lys Ile Leu His Phe Tyr Tyr Leu Ile Met Ser Lys
485 490 495

Gly Lys Ile Val Lys Thr Gly Arg Glu Pro Arg Glu Pro Gly Gln Gly
500 505 510

Leu Phe Ser Leu Ser Ile Pro Val Thr Pro Asp Leu Ala Pro Ser Phe
515 520 525

Arg Leu Val Ala Tyr Tyr Ile Leu Pro Gln Gly Glu Val Val Ala Asp
530 535 540

Ser Val Trp Ile Asp Val Glu Asp Cys Cys Ala Asn Lys Leu Asp Leu
545 550 555 560

Ser Phe Ser Pro Ser Lys Asp Tyr Arg Leu Pro Ala Gln Gln Val Lys
565 570 575

Cura 468 SEQ list 0705

Leu Arg Val Glu Ala Asp Pro Gln Ser Leu Val Ala Leu Arg Ala Val
580 585 590

Asp Gln Ala Val Tyr Leu Leu Lys Pro Lys Ala Lys Leu Ser Met Ser
595 600 605

Lys Val Tyr Asp Leu Leu Glu Lys Ser Asp Leu Gly
610 615 620

<210> 82

<211> 186

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Sodium Bile
acid symporter family consensus sequence

<400> 82

Ala Leu Gly Leu Phe Leu Met Met Phe Ser Met Gly Leu Lys Val Arg
1 5 10 15

Phe Glu Asp Leu Lys Glu Ala Leu Arg Arg Pro Lys Ala Leu Ile Leu
20 25 30

Gly Leu Leu Leu Gln Trp Ile Ile Met Pro Leu Leu Met Phe Ile Leu
35 40 45

Ala Trp Leu Leu Leu Arg Leu Pro Pro Glu Leu Ala Thr Gly Leu Ile
50 55 60

Leu Val Gly Cys Ala Pro Gly Gly Ala Met Ser Asn Val Trp Thr Tyr
65 70 75 80

Leu Ala Lys Gly Asp Val Glu Leu Ser Val Val Met Val Ala Leu Ser
85 90 95

Thr Leu Leu Ala Pro Leu Val Thr Pro Leu Leu Ser Phe Leu Leu Ala
100 105 110

Gly Leu Leu Val His Val Asp Ala Val Ser Pro Trp Ser Leu Ile Lys
115 120 125

Ser Val Leu Val Tyr Val Ile Ile Pro Leu Ile Ala Gly Met Leu Thr
130 135 140

Arg Tyr Phe Leu Pro Glu Trp Phe Glu Gln Arg Val Leu Pro Val Leu
145 150 155 160

Ser Pro Ile Ser Leu Ile Gly Leu Leu Leu Thr Ile Val Val Ile Phe
165 170 175

Ala Leu Asn Gly Glu Val Ile Ala Ser Leu
180 185

<210> 83

<211> 191

<212> PRT

<213> Artificial Sequence

<220>

Cura 468 SEQ list 0705

<223> Description of Artificial Sequence: SPFH
domain/Band 7 family Consensus Sequence

<400> 83

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Val Ala Leu Leu Ile Ile Ile Ala Leu Val Val Ile Ala Met Ser Val
 1          5          10          15
Lys Ile Val Lys Glu Tyr Glu Arg Gly Val Ile Phe Arg Leu Gly Arg
 20          25          30
Tyr Val Arg Gln Val Val Gly Pro Gly Leu His Phe Ile Ile Pro Phe
 35          40          45
Ile Asp Thr Val Lys Lys Val Asp Leu Arg Thr Val Val Tyr Asp Val
 50          55          60
Pro Ser Gln Glu Ile Ile Thr Lys Asp Asn Val Val Val Ile Val Asp
 65          70          75          80
Ala Val Val Tyr Tyr Arg Val Val Asp Pro Leu Lys Ala Val Tyr Glu
 85          90          95
Val Glu Asp Ala Glu Arg Ala Leu Pro Gln Leu Ala Gln Thr Thr Leu
100          105          110
Arg Asn Val Ile Gly Gln Phe Thr Leu Asp Glu Ile Leu Thr Glu Arg
115          120          125
Glu Arg Ile Asn Ser Gln Leu Arg Glu Ile Leu Asp Glu Ala Thr Asp
130          135          140
Pro Trp Gly Ile Lys Val Glu Arg Val Glu Ile Lys Asp Ile Arg Leu
145          150          155          160
Pro Glu Glu Val Gln Arg Ala Met Ala Ala Gln Met Glu Ala Glu Arg
165          170          175
Glu Ala Arg Ala Lys Ile Leu Glu Ala Glu Gly Glu Gln Glu Ala
180          185          190

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<210> 84

<211> 160

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Prohibitin
homologues Consensus Sequence

<400> 84

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Ala Ala Phe Tyr Val Ile Gly Glu Gly Glu Arg Gly Val Val Glu Arg
 1          5          10          15
Leu Gly Arg Val Leu Lys Val Leu Gly Pro Gly Leu His Phe Val Ile
 20          25          30
Pro Phe Ile Asp Asp Val Lys Arg Val Asp Leu Arg Ala Gln Thr Asp
 35          40          45
Asp Val Pro Pro Gln Glu Val Ile Thr Lys Asp Asn Val Thr Val Ser
 50          55          60

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Cura 468 SEQ list 0705

Val Asp Ala Val Val Tyr Tyr Arg Val Leu Asp Pro Leu Lys Ala Val
65 70 75 80
Tyr Gly Val Leu Asp Ala Asp Tyr Arg Ala Leu Arg Gln Leu Ala Gln
85 90 95
Thr Thr Leu Arg Ser Val Ile Gly Lys Arg Thr Leu Asp Glu Leu Leu
100 105 110
Thr Asp Glu Arg Glu Lys Ile Ser Glu Asn Ile Arg Glu Glu Leu Asn
115 120 125
Glu Ala Ala Glu Pro Trp Gly Ile Glu Val Glu Asp Val Glu Ile Lys
130 135 140
Asp Ile Arg Leu Pro Glu Glu Ile Lys Glu Ala Met Glu Ala Gln Gln
145 150 155 160

<210> 85
<211> 79
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Kringle domain
Consensus Sequence

<400> 85
Cys Tyr His Gly Asn Gly Glu Asn Tyr Arg Gly Thr Ala Ser Thr Thr
1 5 10 15
Glu Ser Gly Ala Pro Cys Gln Arg Trp Asp Ser Gln Thr Pro His Arg
20 25 30
His Ser Lys Tyr Thr Pro Glu Arg Tyr Pro Ala Lys Gly Leu Gly Glu
35 40 45
Asn Tyr Cys Arg Asn Pro Asp Gly Asp Glu Arg Pro Trp Cys Tyr Thr
50 55 60
Thr Asp Pro Arg Val Arg Trp Glu Tyr Cys Asp Ile Pro Arg Cys
65 70 75

<210> 86
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Kringle domain
Consensus Sequence

<400> 86
Arg Asp Cys Tyr Ala Gly Asn Gly Glu Ser Tyr Arg Gly Thr Ala Ser
1 5 10 15
Thr Thr Lys Ser Gly Lys Pro Cys Gln Arg Trp Asp Ser Gln Thr Pro
20 25 30

Cura 468 SEQ list 0705

His Leu His Arg Phe Thr Pro Glu Arg Phe Pro Glu Leu Gly Leu Glu
 35 40 45
 His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ser Glu Gly Pro Trp Cys
 50 55 60
 Tyr Thr Thr Asp Pro Asn Val Arg Trp Glu Tyr Cys Asp Ile Pro Gln
 65 70 75 80
 Cys Glu Ser

<210> 87
 <211> 230
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Trypsin-like
 serine protease Consensus Sequence

<400> 87
 Arg Ile Val Gly Gly Ser Glu Ala Asn Ile Gly Ser Phe Pro Trp Gln
 1 5 10 15
 Val Ser Leu Gln Tyr Arg Gly Gly Arg His Phe Cys Gly Gly Ser Leu
 20 25 30
 Ile Ser Pro Arg Trp Val Leu Thr Ala Ala His Cys Val Tyr Gly Ser
 35 40 45
 Ala Pro Ser Ser Ile Arg Val Arg Leu Gly Ser His Asp Leu Ser Ser
 50 55 60
 Gly Glu Glu Thr Gln Thr Val Lys Val Ser Lys Val Ile Val His Pro
 65 70 75 80
 Asn Tyr Asn Pro Ser Thr Tyr Asp Asn Asp Ile Ala Leu Leu Lys Leu
 85 90 95
 Ser Glu Pro Val Thr Leu Ser Asp Thr Val Arg Pro Ile Cys Leu Pro
 100 105 110
 Ser Ser Gly Tyr Asn Val Pro Ala Gly Thr Thr Cys Thr Val Ser Gly
 115 120 125
 Trp Gly Arg Thr Ser Glu Ser Ser Gly Ser Leu Pro Asp Thr Leu Gln
 130 135 140
 Glu Val Asn Val Pro Ile Val Ser Asn Ala Thr Cys Arg Arg Ala Tyr
 145 150 155 160
 Ser Gly Gly Pro Ala Ile Thr Asp Asn Met Leu Cys Ala Gly Gly Leu
 165 170 175
 Glu Gly Gly Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val
 180 185 190
 Cys Asn Asp Pro Arg Trp Val Leu Val Gly Ile Val Ser Trp Gly Ser
 195 200 205

Cura 468 SEQ list 0705

Tyr Gly Cys Ala Arg Pro Asn Lys Pro Gly Val Tyr Thr Arg Val Ser
210 215 220

Ser Tyr Leu Asp Trp Ile
225 230

<210> 88
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Trypsin
Consensus Sequence

<400> 88
Ile Val Gly Gly Arg Glu Ala Gln Ala Gly Ser Phe Pro Trp Gln Val
1 5 10 15
Ser Leu Gln Val Ser Ser Gly His Phe Cys Gly Gly Ser Leu Ile Ser
20 25 30
Glu Asn Trp Val Leu Thr Ala Ala His Cys Val Ser Gly Ala Ser Ser
35 40 45
Val Arg Val Val Leu Gly Glu His Asn Leu Gly Thr Thr Glu Gly Thr
50 55 60
Glu Gln Lys Phe Asp Val Lys Lys Ile Ile Val His Pro Asn Tyr Asn
65 70 75 80
Pro Asp Thr Asn Asp Ile Ala Leu Leu Lys Leu Lys Ser Pro Val Thr
85 90 95
Leu Gly Asp Thr Val Arg Pro Ile Cys Leu Pro Ser Ala Ser Ser Asp
100 105 110
Leu Pro Val Gly Thr Thr Cys Ser Val Ser Gly Trp Gly Arg Thr Lys
115 120 125
Asn Leu Gly Thr Ser Asp Thr Leu Gln Glu Val Val Val Pro Ile Val
130 135 140
Ser Arg Glu Thr Cys Arg Ser Ala Tyr Gly Gly Thr Val Thr Asp Thr
145 150 155 160
Met Ile Cys Ala Gly Ala Leu Gly Gly Lys Asp Ala Cys Gln Gly Asp
165 170 175
Ser Gly Gly Pro Leu Val Cys Ser Asp Gly Glu Leu Val Gly Ile Val
180 185 190
Ser Trp Gly Tyr Gly Cys Ala Val Gly Asn Tyr Pro Gly Val Tyr Thr
195 200 205
Arg Val Ser Arg Tyr Leu Asp Trp Ile
210 215

<210> 89
<211> 79
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Divergent
subfamily of APPLE domains Consensus Sequence

<400> 89

Lys Ser Asp Asp Cys Phe Val Arg Leu Pro Asn Thr Lys Leu Pro Asp
1 5 10 15
Phe Ser Pro Ile Val Ile Ser Val Ala Ser Leu Glu Glu Cys Ala Gln
20 25 30
Lys Cys Leu Asn Ser Asn Cys Ser Cys Arg Ser Phe Thr Tyr Asn Asn
35 40 45
Asp Thr Lys Gly Cys Leu Leu Trp Ser Glu Ser Ser Leu Gly Asp Ala
50 55 60
Arg Gln Leu Leu Pro Ser Gly Gly Val Asp Tyr Tyr Glu Lys Ile
65 70 75

<210> 90

<211> 145

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Lipocalin/cytosolic fatty-acid binding protein
family Consensus Sequence

<400> 90

Lys Phe Ala Gly Lys Trp Tyr Leu Val Ala Ser Ala Asn Phe Asp Pro
1 5 10 15
Glu Leu Lys Glu Glu Leu Gly Val Leu Glu Ala Thr Arg Lys Glu Ile
20 25 30
Thr Pro Leu Lys Glu Gly Asn Leu Glu Ile Val Phe Asp Gly Asp Lys
35 40 45
Asn Gly Ile Cys Glu Glu Thr Phe Gly Lys Leu Glu Lys Thr Lys Lys
50 55 60
Leu Gly Val Glu Phe Asp Tyr Tyr Thr Gly Asp Asn Arg Phe Val Val
65 70 75 80
Leu Asp Thr Asp Tyr Asp Asn Tyr Leu Leu Val Cys Val Gln Lys Gly
85 90 95
Asp Gly Asn Glu Thr Ser Arg Thr Ala Glu Leu Tyr Gly Arg Thr Pro
100 105 110
Glu Leu Ser Pro Glu Ala Leu Glu Leu Phe Glu Thr Ala Thr Lys Glu
115 120 125
Leu Gly Ile Pro Glu Asp Asn Val Val Cys Thr Arg Gln Thr Glu Arg
130 135 140
Cys
145

Cura 468 SEQ list 0705

<210> 91
 <211> 218
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Connexin
 Consensus Sequence

<400> 91
 Met Asp Trp Ser Phe Leu Gly Arg Leu Leu Glu Gly Val Asn Lys His
 1 5 10 15
 Ser Thr Ala Ile Gly Lys Ile Trp Leu Ser Val Leu Phe Ile Phe Arg
 20 25 30
 Ile Leu Val Leu Gly Val Ala Ala Glu Ser Val Trp Gly Asp Glu Gln
 35 40 45
 Ser Asp Phe Val Cys Asn Thr Gln Gln Pro Gly Cys Glu Asn Val Cys
 50 55 60
 Tyr Asp Gln Phe Phe Pro Ile Ser His Val Arg Leu Trp Val Leu Gln
 65 70 75 80
 Leu Ile Phe Val Ser Thr Pro Ser Leu Leu Tyr Leu Gly His Val Ala
 85 90 95
 Tyr Arg Val Arg Arg Glu Glu Lys Leu Arg Glu Lys Glu Glu Glu His
 100 105 110
 Ser Lys Gly Leu Tyr Ser Glu Glu Ala Lys Lys Arg Cys Gly Ser Glu
 115 120 125
 Asp Gly Lys Val Arg Ile Arg Gly Gly Leu Trp Trp Thr Tyr Val Phe
 130 135 140
 Ser Ile Ile Phe Lys Ser Ile Phe Glu Val Gly Phe Leu Tyr Gly Gln
 145 150 155 160
 Tyr Leu Leu Tyr Gly Phe Thr Met Ser Pro Leu Val Val Cys Ser Arg
 165 170 175
 Ala Pro Cys Pro His Thr Val Asp Cys Phe Val Ser Arg Pro Thr Glu
 180 185 190
 Lys Thr Ile Phe Ile Val Phe Met Leu Val Val Ser Ala Ile Cys Leu
 195 200 205
 Leu Leu Asn Leu Ala Glu Leu Phe Tyr Leu
 210 215

<210> 92
 <211> 59
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Src homology 3
 domains Consensus Sequence

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<400> 92

Glu Gly Pro Gln Val Arg Ala Leu Tyr Asp Tyr Thr Ala Gln Asp Pro
 1 5 10 15
 Asp Glu Leu Ser Phe Lys Lys Gly Asp Ile Ile Thr Val Leu Glu Lys
 20 25 30
 Ser Asp Asp Gly Trp Trp Lys Gly Arg Leu Gly Thr Gly Lys Glu Gly
 35 40 45
 Leu Phe Pro Ser Asn Tyr Val Glu Glu Ile Asp
 50 55

<210> 93

<211> 57

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: SH3 domain
 Consensus Sequence

<400> 93

Pro Lys Val Val Ala Leu Tyr Asp Tyr Gln Ala Arg Glu Ser Asp Glu
 1 5 10 15
 Leu Ser Phe Lys Lys Gly Asp Ile Ile Ile Val Leu Glu Lys Ser Asp
 20 25 30
 Asp Gly Gly Trp Trp Lys Gly Arg Leu Lys Gly Thr Lys Glu Gly Leu
 35 40 45
 Ile Pro Ser Asn Tyr Val Glu Pro Val
 50 55

<210> 94

<211> 91

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fes/CIP4
 homology domain Consensus Sequence

<400> 94

Met Gly Phe Trp Ser Glu Leu Asp Asp Gly Phe Glu Ala Leu Leu Ser
 1 5 10 15
 Arg Leu Lys Asn Gly Leu Arg Leu Leu Glu Asp Leu Lys Lys Phe Met
 20 25 30
 Arg Glu Arg Ala Lys Ile Glu Glu Glu Tyr Ala Lys Lys Leu Gln Lys
 35 40 45
 Leu Ser Lys Lys Leu Arg Ala Val Arg Asp Thr Glu Ser Glu Leu Gly
 50 55 60
 Ser Leu Arg Lys Ala Trp Glu Val Leu Leu Ser Glu Thr Asp Ala Leu
 65 70 75 80

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Ala Lys Gln His Leu Gln Leu Ser Glu Asp Leu
85 90

<210> 95

<211> 94

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fes/CIP4
homology domain Consensus Sequence

<400> 95

Met Gly Phe Gly Ser Glu Leu Cys Pro Glu Gly His Lys Ala Leu Leu
1 5 10 15

Ser Arg Gln Asp Asn Glu Leu Arg Leu Leu Glu Glu Met Lys Lys Phe
20 25 30

Met Ala Glu Arg Ala Lys Ile Glu Lys Glu Tyr Ala Gly Lys Leu Gln
35 40 45

His Leu Ser Ala Gln Val Gly Lys Gly Pro Ala Thr Ala Glu Gly Glu
50 55 60

Asp Glu Leu Ser Ser Leu Lys Ser Trp Ala Val Ile Leu Ser Glu Thr
65 70 75 80

Glu Gln Gln Ser Lys Ile His Leu Gln Ile Ser Glu Asp Leu
85 90

<210> 96

<211> 230

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Trypsin-like
serine protease Consensus Sequence

<400> 96

Arg Ile Val Gly Gly Ser Glu Ala Asn Ile Gly Ser Phe Pro Trp Gln
1 5 10 15

Val Ser Leu Gln Tyr Arg Gly Gly Arg His Phe Cys Gly Gly Ser Leu
20 25 30

Ile Ser Pro Arg Trp Val Leu Thr Ala Ala His Cys Val Tyr Gly Ser
35 40 45

Ala Pro Ser Ser Ile Arg Val Arg Leu Gly Ser His Asp Leu Ser Ser
50 55 60

Gly Glu Glu Thr Gln Thr Val Lys Val Ser Lys Val Ile Val His Pro
65 70 75 80

Asn Tyr Asn Pro Ser Thr Tyr Asp Asn Asp Ile Ala Leu Leu Lys Leu
85 90 95

Ser Glu Pro Val Thr Leu Ser Asp Thr Val Arg Pro Ile Cys Leu Pro
100 105 110

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Ser Ser Gly Tyr Asn Val Pro Ala Gly Thr Thr Cys Thr Val Ser Gly
115 120 125
Trp Gly Arg Thr Ser Glu Ser Ser Gly Ser Leu Pro Asp Thr Leu Gln
130 135 140
Glu Val Asn Val Pro Ile Val Ser Asn Ala Thr Cys Arg Arg Ala Tyr
145 150 155 160
Ser Gly Gly Pro Ala Ile Thr Asp Asn Met Leu Cys Ala Gly Gly Leu
165 170 175
Glu Gly Gly Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val
180 185 190
Cys Asn Asp Pro Arg Trp Val Leu Val Gly Ile Val Ser Trp Gly Ser
195 200 205
Tyr Gly Cys Ala Arg Pro Asn Lys Pro Gly Val Tyr Thr Arg Val Ser
210 215 220
Ser Tyr Leu Asp Trp Ile
225 230

<210> 97

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Trypsin
Consensus Sequence

<400> 97

Ile Val Gly Gly Arg Glu Ala Gln Ala Gly Ser Phe Pro Trp Gln Val
1 5 10 15
Ser Leu Gln Val Ser Ser Gly His Phe Cys Gly Gly Ser Leu Ile Ser
20 25 30
Glu Asn Trp Val Leu Thr Ala Ala His Cys Val Ser Gly Ala Ser Ser
35 40 45
Val Arg Val Val Leu Gly Glu His Asn Leu Gly Thr Thr Glu Gly Thr
50 55 60
Glu Gln Lys Phe Asp Val Lys Lys Ile Ile Val His Pro Asn Tyr Asn
65 70 75 80
Pro Asp Thr Asn Asp Ile Ala Leu Leu Lys Leu Lys Ser Pro Val Thr
85 90 95
Leu Gly Asp Thr Val Arg Pro Ile Cys Leu Pro Ser Ala Ser Ser Asp
100 105 110
Leu Pro Val Gly Thr Thr Cys Ser Val Ser Gly Trp Gly Arg Thr Lys
115 120 125
Asn Leu Gly Thr Ser Asp Thr Leu Gln Glu Val Val Val Pro Ile Val
130 135 140

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Ser Arg Glu Thr Cys Arg Ser Ala Tyr Gly Gly Thr Val Thr Asp Thr
 145 150 155 160
 Met Ile Cys Ala Gly Ala Leu Gly Gly Lys Asp Ala Cys Gln Gly Asp
 165 170 175
 Ser Gly Gly Pro Leu Val Cys Ser Asp Gly Glu Leu Val Gly Ile Val
 180 185 190
 Ser Trp Gly Tyr Gly Cys Ala Val Gly Asn Tyr Pro Gly Val Tyr Thr
 195 200 205
 Arg Val Ser Arg Tyr Leu Asp Trp Ile
 210 215

<210> 98
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: NOV5 Primer 1

<400> 98
 ctccactcc tgctgcttct gact 24

<210> 99
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: NOV5 Primer 2

<400> 99
 aaggctgggc ctaaccagct ctcac 25

<210> 100
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: NOV7 Primer 1

<400> 100
 catgaactgg gcatttctgc agg 23

<210> 101
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: NOV7 Primer 2

<400> 101
 ttatctgctg atctgcagg ttatgga 27

Cura 468 SEQ list 0705

<210> 102
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: NOV8 Primer 1

 <400> 102
 ctgacaggcc ctggtgtgtg at 22

 <210> 103
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: NOV8 Primer 2

 <400> 103
 tcacacatgt ttcatgtggg agttaga 27

 <210> 104
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: NOV9 Primer 1

 <400> 104
 gagtgagagg tcggacagac tgtg 24

 <210> 105
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: NOV9 Primer 2

 <400> 105
 actcatgcaa cttgcttctc tcactct 27

 <210> 106
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: NOV10b Primer
 1

 <400> 106
 cctatgagcc tgatgctgga tgac 24

 <210> 107

Cura 468 SEQ list 0705

<211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: NOV10b Primer
 2
 <400> 107
 aggactcaga ggagggagtc ctgag 25
 <210> 108
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Ag4164 Forward
 <400> 108
 gcactacaag tggaagcctt ac 22
 <210> 109
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Ag4164 Probe
 <400> 109
 ctcaagtaga agccgactta tgcaaa 26
 <210> 110
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Ag4164 Reverse
 <400> 110
 tcaaatcctt ctgcgataca gt 22
 <210> 111
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Ag1313b
 Forward
 <400> 111
 cagctgcacg attaatgaag at 22
 <210> 112
 <211> 25

Cura 468 SEQ list 0705

<212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Ag1313b Probe
 <400> 112
 aggtcttgga ctggccttca ccatt 25

<210> 113
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Ag1313b
 Reverse
 <400> 113
 ccaaagttgt gtccagactc at 22

<210> 114
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Ag2197 Forward
 <400> 114
 ccaaggaaga cctcttcac tt 22

<210> 115
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Ag2197 Probe
 <400> 115
 tcttgcttac ggcataagcg ctctct 26

<210> 116
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Ag2197 Reverse
 <400> 116
 ttcatttcta tgggacctca ga 22

<210> 117
 <211> 21
 <212> DNA
 <213> Artificial Sequence

Cura 468 SEQ list 0705

<220>
 <223> Description of Artificial Sequence: Ag708 Forward
 <400> 117
 aaagatggga ctcgtcatga c 21
 <210> 118
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Ag708 Probe
 <400> 118
 cacgccatct tactgactgg tctgga 26
 <210> 119
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Ag708 Reverse
 <400> 119
 gtgcaaattcc caaagtgatca 20
 <210> 120
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Ag4164 Forward
 <400> 120
 gcactacaag tggaagcctt ac 22
 <210> 121
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Ag4164 Probe
 <400> 121
 ctcaagtaga agccgactta tgcaaa 26
 <210> 122
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Ag4164 Reverse

Cura 468 SEQ list 0705

<400> 122
tcaaatacctt ctgcgataca gt 22

<210> 123
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag2197 Forward

<400> 123
ccaaggaaga cctcttcatc tt 22

<210> 124
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag2197 Probe

<400> 124
tcttgcttac ggcataagcg ctctct 26

<210> 125
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag2197 Reverse

<400> 125
ttcatttcta tgggacctca ga 22

<210> 126
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag2197 Forward

<400> 126
ccaaggaaga cctcttcatc tt 22

<210> 127
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag2197 Probe

<400> 127
tcttgcttac ggcataagcg ctctct 26

Cura 468 SEQ list 0705

<210> 128
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag2197 Reverse

 <400> 128
 ttcatttcta tgggacctca ga 22

 <210> 129
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag708 Forward

 <400> 129
 aaagatggga ctggtcatga c 21

 <210> 130
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag708 Probe

 <400> 130
 cacgccatct tactgactgg tctgga 26

 <210> 131
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag708 Reverse

 <400> 131
 gtgcaaattcc caaagtgta 20

 <210> 132
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag1313b
 Forward

 <400> 132
 cagctgcacg attaatgaag at 22

Cura 468 SEQ list 0705

<210> 133
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Ag1313b Probe
 <400> 133
 aggtcttgga ctggccttca ccatt 25

<210> 134
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Ag1313b
 Reverse
 <400> 134
 ccaaagttgt gtccagactc at 22

<210> 135
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Ag1537 Forward
 <400> 135
 tttcaagaca ccctgtgata cc 22

<210> 136
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Ag1537 Probe
 <400> 136
 acttcgtgtc ctgaatgttc caggct 26

<210> 137
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Ag1537 Reverse
 <400> 137
 cagaggaatg aaggcataga tg 22

<210> 138
 <211> 21

Cura 468 SEQ list 0705

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag2432 Forward

<400> 138
 gtaggcaaag ggactcactg t 21

<210> 139
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag2432 Probe

<400> 139
 cagaaatcaa taatctttga ctgccg 26

<210> 140
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag2432 Reverse

<400> 140
 gcacattacg tggctgaga 19

<210> 141
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag1250 Forward

<400> 141
 cgtggtgaac tctgccttat at 22

<210> 142
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag1250 Probe

<400> 142
 cacagagctg tcgtctttga ccgatt 26

<210> 143
 <211> 21
 <212> DNA
 <213> Artificial Sequence

Cura 468 SEQ list 0705

<220>
 <223> Description of Artificial Sequence: Ag1250 Reverse
 <400> 143
 agtccctttg cctaccacaa t 21

<210> 144
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag3086 Forward
 <400> 144
 ggacccatt cgactactgt 20

<210> 145
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag3086 Probe
 <400> 145
 ctgatgacca gccgcatca atc 23

<210> 146
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag3086 Reverse
 <400> 146
 ttctcaaact gcacctggtc 20

<210> 147
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag3797 Forward
 <400> 147
 tctggacgac aactattgcc 20

<210> 148
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag3797 Probe

Cura 468 SEQ list 0705

<400> 148
atggtgctac actacggatc cgacg 25

<210> 149
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag3797 Reverse

<400> 149
gtcacagaat tctcgctcga 20

<210> 150
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag2439 Forward

<400> 150
tatcatcact tgtgatggca aa 22

<210> 151
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag2439 Probe

<400> 151
aaaaccgaga gcactttgaa aacaca 26

<210> 152
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag2439 Reverse

<400> 152
aaacttctct cccagggtac aa 22

<210> 153
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag2771 Forward

<400> 153
tgaacagaac tatgcgaaac aa 22

Cura 468 SEQ list 0705

<210> 154
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag2771 Probe

 <400> 154
 tctggttaag aagtactgcc ccaaacg 27

 <210> 155
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag2771 Reverse

 <400> 155
 ggctcttcac ttttgatga a 21

 <210> 156
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag1674 Forward

 <400> 156
 ctactcacc acaaggagat aa 22

 <210> 157
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag1674 Probe

 <400> 157
 tgacatcaaa ctcaacagtt cccagga 27

 <210> 158
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag1674 Reverse

 <400> 158
 gtctaggaga gagctgagca aa 22

 <210> 159
 <211> 78

Cura 468 SEQ list 0705

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PAN domain
Consensus Sequence

<400> 159

Cys Ser Ser Phe Val Arg Val Pro Gly Arg Ser Leu Ser Gly Asn Asp
1 5 10 15

Ile Ser Val Val Asn Val Pro Ser Leu Glu Glu Cys Ala Ala Leu Cys
20 25 30

Leu Glu Glu Pro Arg Val Cys Arg Ser Phe Thr Tyr Asn Asn Lys Ser
35 40 45

Lys Gln Cys Leu Leu Lys Ser Glu Ser Ser Gly Ser Leu Pro Arg Leu
50 55 60

Lys Arg Pro Ser Gln Lys Val Asp Tyr Tyr Glu Lys Ser Cys
65 70 75

<210> 160

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Connexin
homologues Consensus Sequence

<400> 160

Ser Val Trp Gly Asp Glu Gln Ser Asp Phe Thr Cys Asn Thr Gln Gln
1 5 10 15

Pro Gly Cys Glu Asn Val Cys Tyr Asp Gln Phe Phe Pro Ile Ser His
20 25 30

Val Arg

<210> 161

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

<400> 161

Asn Glu Gln Lys
1

<210> 162

<211> 4

<212> PRT

<213> Artificial Sequence

Cura 468 SEQ list 0705

<220>
<223> Description of Artificial Sequence:

<400> 162

Asn His Gln Lys
1

<210> 163
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:

<400> 163

Asn Asp Glu Gln
1

<210> 164
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:

<400> 164

Gln His Arg Lys
1

<210> 165
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:

<400> 165

Met Ile Leu Val
1

<210> 166
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:

Cura 468 SEQ list 0705

<400> 166

Met Ile Leu Phe
1